



# STIC SEARCH RESULTS

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor  
308-4258, CM1-1E01

## Voluntary Results Feedback Form

➤ I am an examiner in Workgroup:  Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library/CM1- Circ. Desk



**THIS PAGE BLANK (USPTO)**



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 97246**

**TO: Nita M Minnifield  
Location: 1/8a07 & 8e12  
Art Unit: 1645  
Tuesday, June 24, 2003**

**Case Serial Number: 002784**

**From: Edward Hart  
Location: Biotech-Chem Library  
CM1-6B02  
Phone: 305-9203**

**edward.hart@uspto.gov**

### **Search Notes**

Examiner Minnifield,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

**THIS PAGE BLANK (USPTO)**



97245  
**STIC-Biotech/ChemLib**

---

**From:** Chan, Christina  
**Sent:** Monday, June 23, 2003 1:16 PM  
**To:** Minnifield, Nita; STIC-Biotech/ChemLib  
**Subject:** RE: rush sequence search

**Please rush. Thanks Chris**

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

-----Original Message-----

**From:** Minnifield, Nita  
**Sent:** Monday, June 23, 2003 12:47 PM  
**To:** Chan, Christina  
**Subject:** rush sequence search

Christina, please approve, 2 month amdt.

STIC

10/002784

Please do a commercial database search on SEQ ID NO: 16 and 27.

Please provide paper copy of the results.

Thanks,  
Nita M. Minnifield  
Art Unit 1645  
Office CM1-8A07  
Mailbox CM1-8E12  
703-305-3394

Edward Hart  
Technical Info. Specialist  
STIC/Biotech  
CMI 6B02 Tel: 305-9203

6/23/03  
ABSSOR  
2-AA

**THIS PAGE BLANK (USPTO)**

## WEST Search History

DATE: Tuesday, June 24, 2003

<u>Set Name</u> side by side	<u>Query</u>	<u>Hit Count</u>	<u>Set Name</u> result set
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=ADJ</i>			
L11	I5 and pyrogenic:adj5 exotoxin	18	L11
L10	L5 and pyrogenic	18	L10
L9	I7 and altered adj10 antigen receptor	4	L9
L8	L7 and altered adj10 class II	4	L8
L7	I5 and streptococc\$	77	L7
L6	L5 and streptococc?	13	L6
L5	bacterial adj5 superantigen	197	L5
L4	L3 and superantigen	3	L4
L3	I1 or L2	29	L3
L2	ulrich-robert-g.in.	3	L2
L1	ulrich-robert.in.	26	L1

END OF SEARCH HISTORY

**THIS PAGE BLANK (USPTO)**

WEST

Generate Collection

Print

## Search Results - Record(s) 1 through 4 of 4 returned.

☐ 1. Document ID: US 20030036644 A1

L8: Entry 1 of 4

File: PGPB

Feb 20, 2003

PGPUB-DOCUMENT-NUMBER: 20030036644  
PGPUB-FILING-TYPE: new  
DOCUMENT-IDENTIFIER: US 20030036644 A1

TITLE: Bacterial superantigen vaccines

PUBLICATION-DATE: February 20, 2003

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ulrich, Robert G.	Frederick	MD	US	

US-CL-CURRENT: 536/23.1; 536/23.7

File | Title | Claims | Front | Reverse | Classification | Date | Reference | Sequence | Abstracts | Claims | Date | Date | Date | Date

☐ 2. Document ID: US 20030009015 A1

L8: Entry 2 of 4

File: PGPB

Jan 9, 2003

PGPUB-DOCUMENT-NUMBER: 20030009015  
PGPUB-FILING-TYPE: new  
DOCUMENT-IDENTIFIER: US 20030009015 A1

TITLE: BACTERIAL SUPERANTIGEN VACCINES

PUBLICATION-DATE: January 9, 2003

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
ULRICH, ROBERT G.	FREDERICK	MD	US	
OLSON, MARK A.	GAITHERSBURG	MD	US	
BAVARI, SINA	DILLSBURG	PA	US	

US-CL-CURRENT: 536/23.1; 424/184.1, 435/320.1

File | Title | Claims | Front | Reverse | Classification | Date | Reference | Sequence | Abstracts | Claims | Date | Date | Date | Date

File | Title | Claims | Front | Reverse | Classification | Date | Reference | Sequence | Abstracts | Claims | Date | Date | Date | Date

☐ 3. Document ID: US 6399332 B1

L8: Entry 3 of 4

File: USPT

Jun 4, 2002

US-PAT-NO: 6399332  
DOCUMENT-IDENTIFIER: US 6399332 B1

**THIS PAGE BLANK (USPTO)**

TITLE: Bacterial superantigen vaccines

DATE-ISSUED: June 4, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ulrich; Robert G.	Frederick	MD		
Olson; Mark A.	Gaithersburg	MD		
Bavari; Sina	Dillsburg	PA		

US-CL-CURRENT: 435/69.3; 435/252.3; 435/252.33; 435/320.1; 435/325; 435/69.1,  
435/71.1; 435/71.3; 536/23.1; 536/23.7

Full | Title | Patent | Front | Reverse | Classification | Date | References | Sequences | Attachments

Image | Draw Desc | Image

☐ 4. Document ID: JP 2002522055 W WO 200009154 A1 AU 9889049 A EP 1105154 A1

L8: Entry 4 of 4

File: DWPI

Jul 23, 2002

DERWENT-ACC-NO: 2000-224177

DERWENT-WEEK: 200263

COPYRIGHT 2003 DERWENT INFORMATION LTD

TITLE: Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections

INVENTOR: BAVARI, S; OLSON, M A ; ULRICH, R G

PRIORITY-DATA: 1998WO-US16766 (August 13, 1998)

## PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
JP 2002522055 W	July 23, 2002		103	C12N015/09
WO 200009154 A1	February 24, 2000	E	118	A61K039/00
AU 9889049 A	March 6, 2000		000	A61K039/00
EP 1105154 A1	June 13, 2001	E	000	A61K039/00

INT-CL (IPC): A61 K 39/00; A61 K 39/02; A61 K 39/085; A61 K 39/09; A61 K 39/44; A61 P 31/00; A61 P 35/00; A61 P 37/04; C07 K 14/00; C07 K 14/31; C12 N 1/20; C12 N 1/21; C12 N 15/00; C12 N 15/09; C12 N 15/63; C12 P 21/00; C12 P 21/02; G01 N 33/53; G01 N 33/569

Full | Title | Patent | Front | Reverse | Classification | Date | References | Sequences | Attachments

Image | Draw Desc | Image

Generate Collection

Print

**THIS PAGE BLANK (USPTO)**



Term	Documents
ALTERED	229335
ALTEREDS	0
CLASS	289019
CLASSES	110796
II	1492271
IIS	1903
(7 AND (ALTERED ADJ10 CLASS ADJ II)). USPT,PGPB,JPAB,EPAB,DWPI,TDBD.	4
(L7 AND ALTERED ADJ10 CLASS II). USPT,PGPB,JPAB,EPAB,DWPI,TDBD.	4

Display Format:

[Previous Page](#)   [Next Page](#)

**THIS PAGE BLANK (USPTO)**

**WEST**[Generate Collection](#)[Print](#)**Search Results - Record(s) 1 through 18 of 18 returned.**☐ 1. Document ID: US 20030092894 A1

L11: Entry 1 of 18

File: PGPB

May 15, 2003

PGPUB-DOCUMENT-NUMBER: 20030092894  
PGPUB-FILING-TYPE: new  
DOCUMENT-IDENTIFIER: US 20030092894 A1

TITLE: Modified chimeric superantigens and their use

PUBLICATION-DATE: May 15, 2003

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Antonsson, Per	Lund		SE	
Bjork, Per	Helsingborg		SE	
Dohlsten, Mikael	Lund		SE	
Kalland, Terje	Arese		IT	
Hansson, Johan	Lund		SE	
Forsberg, Goran	Lund		SE	
Abrahmsen, Lars	Bromma		SE	

US-CL-CURRENT: 530/388.1; 435/7.23, 530/388.8[Full](#) | [Info](#) | [Citation](#) | [Front](#) | [Figure](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequences](#) | [Attachments](#)[Table](#) | [Open Data](#) | [Image](#)☐ 2. Document ID: US 20030036644 A1

L11: Entry 2 of 18

File: PGPB

Feb 20, 2003

PGPUB-DOCUMENT-NUMBER: 20030036644  
PGPUB-FILING-TYPE: new  
DOCUMENT-IDENTIFIER: US 20030036644 A1

TITLE: Bacterial superantigen vaccines

PUBLICATION-DATE: February 20, 2003

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ulrich, Robert G.	Frederick	MD	US	

US-CL-CURRENT: 536/23.1; 536/23.7[Full](#) | [Info](#) | [Citation](#) | [Front](#) | [Figure](#) | [Classification](#) | [Date](#) | [Reference](#) | [Sequences](#) | [Attachments](#)[Table](#) | [Open Data](#) | [Image](#)☐ 3. Document ID: US 20030009015 A1

**2 PAGE BLANK (USPTO)**

L11: Entry 3 of 18

File: PGPB

Jan 9, 2003

PGPUB-DOCUMENT-NUMBER: 20030009015  
PGPUB-FILING-TYPE: new  
DOCUMENT-IDENTIFIER: US 20030009015 A1

TITLE: BACTERIAL SUPERANTIGEN VACCINES

PUBLICATION-DATE: January 9, 2003

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
ULRICH, ROBERT G.	FREDERICK	MD	US	
OLSON, MARK A.	GAITHERSBURG	MD	US	
BAVARI, SINA	DILLSBURG	PA	US	

US-CL-CURRENT: 536/23.1; 424/184.1, 435/320.1

File | Title | Creation | Print | Review | Classification | Date | Reference | Sequences | Attachments

Help | View Desc | Help

☐ 4. Document ID: US 20020197234 A1

L11: Entry 4 of 18

File: PGPB

Dec 26, 2002

PGPUB-DOCUMENT-NUMBER: 20020197234  
PGPUB-FILING-TYPE: new  
DOCUMENT-IDENTIFIER: US 20020197234 A1

TITLE: Immunologic activities of rhesus cytomegalovirus encoded IL-10 and human cytomegalovirus encoded IL-10

PUBLICATION-DATE: December 26, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Schall, Thomas J.	Menlo Park	CA	US	
Penfold, Mark	Mountain View	CA	US	
Spencer, Juliet	Foster City	CA	US	

US-CL-CURRENT: 424/85.2; 424/93.7, 435/372

File | Title | Creation | Print | Review | Classification | Date | Reference | Sequences | Attachments

Help | View Desc | Help

☐ 5. Document ID: US 6514498 B1

L11: Entry 5 of 18

File: USPT

Feb 4, 2003

US-PAT-NO: 6514498  
DOCUMENT-IDENTIFIER: US 6514498 B1

TITLE: Modified/chimeric superantigens and their use

DATE-ISSUED: February 4, 2003

## INVENTOR-INFORMATION:

**THIS PAGE BLANK (USPTO)**

NAME	CITY	STATE	ZIP CODE	COUNTRY
Antonsson; Per	Lund			SE
Bjork; Per	Helsingborg			SE
Dohlsten; Mikael	Lund			SE
Hansson; Johan	Lund			SE
Forsberg; Goran	Lund			SE
Abrahmsen; Lars	Bromma			SE
Kalland; Terje	Arese			IT

US-CL-CURRENT: 424/178.1, 424/182.1, 424/184.1, 424/185.1, 424/190.1, 424/192.1,  
424/194.1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequence | Attachments

View | Draw Data | Image

☐ 6. Document ID: US 6447777 B1

L11: Entry 6 of 18

File: USPT

Sep 10, 2002

US-PAT-NO: 6447777

DOCUMENT-IDENTIFIER: US 6447777 B1

TITLE: Polymerized staphylococcal protein a for treatment of diseases

DATE-ISSUED: September 10, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David Stephen	Pebble Beach	CA		
Reiser; Raoul F.	Sarasota	FL		

US-CL-CURRENT: 424/184.1, 424/236.1, 424/237.1, 424/243.1, 424/280.1, 514/12,  
514/18, 530/350, 530/387.1

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequence | Attachments

View | Draw Data | Image

☐ 7. Document ID: US 6399332 B1

L11: Entry 7 of 18

File: USPT

Jun 4, 2002

US-PAT-NO: 6399332

DOCUMENT-IDENTIFIER: US 6399332 B1

TITLE: Bacterial superantigen vaccines

DATE-ISSUED: June 4, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ulrich; Robert G.	Frederick	MD		
Olson; Mark A.	Gaithersburg	MD		
Bavari; Sina	Dillsburg	PA		

US-CL-CURRENT: 435/69.3, 435/252.3, 435/252.33, 435/320.1, 435/325, 435/69.1,  
435/71.1, 435/71.3, 536/23.1, 536/23.7

**THIS PAGE BLANK (USPTO)**



Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments

View | Draw Data | Image

☐ 8. Document ID: US 6340461 B1

L11: Entry 8 of 18

File: USPT

Jan 22, 2002

US-PAT-NO: 6340461

DOCUMENT-IDENTIFIER: US 6340461 B1

TITLE: Superantigen based methods and compositions for treatment of diseases

DATE-ISSUED: January 22, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David Stephen	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/193.1; 424/192.1, 424/194.1, 424/277.1, 424/278.1, 424/280.1,  
424/282.1, 435/68.1, 435/69.1, 435/69.3, 435/69.7

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments

View | Draw Data | Image

☐ 9. Document ID: US 6338845 B1

L11: Entry 9 of 18

File: USPT

Jan 15, 2002

US-PAT-NO: 6338845

DOCUMENT-IDENTIFIER: US 6338845 B1

TITLE: Tumor killing effects of enterotoxins, superantigens, and related compounds

DATE-ISSUED: January 15, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/93.1; 424/93.2, 424/93.21, 424/93.7, 424/93.71, 435/372,  
435/372.1, 435/372.2, 435/372.3

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments

View | Draw Data | Image

☐ 10. Document ID: US 6251385 B1

L11: Entry 10 of 18

File: USPT

Jun 26, 2001

US-PAT-NO: 6251385

DOCUMENT-IDENTIFIER: US 6251385 B1

TITLE: Method of cancer treatment

DATE-ISSUED: June 26, 2001

## INVENTOR-INFORMATION:

**THIS PAGE BLANK (USPTO)**

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/93.7; 424/184.1, 424/236.1, 424/237.1, 424/277.1, 424/93.1,  
424/93.2, 424/93.71, 435/325

Full Title Citation Front Review Classification Date Reference Sequences Attachments

View Draw Desc Image

☐ 11. Document ID: US 6221351 B1

L11: Entry 11 of 18

File: USPT

Apr 24, 2001

US-PAT-NO: 6221351

DOCUMENT-IDENTIFIER: US 6221351 B1

TITLE: Tumor killing effects of enterotoxins, superantigens, and related compounds

DATE-ISSUED: April 24, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/93.71; 424/93.1, 424/93.2, 424/93.21, 424/93.7, 435/69.3, 514/44,  
530/395

Full Title Citation Front Review Classification Date Reference Sequences Attachments

View Draw Desc Image

☐ 12. Document ID: US 6126945 A

L11: Entry 12 of 18

File: USPT

Oct 3, 2000

US-PAT-NO: 6126945

DOCUMENT-IDENTIFIER: US 6126945 A

TITLE: Tumor killing effects of enterotoxins, superantigens, and related compounds

DATE-ISSUED: October 3, 2000

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA		
Stone; Jay L.	Aptos	CA		

US-CL-CURRENT: 424/237.1; 424/236.1, 424/243.1, 424/244.1, 435/69.1, 435/69.3,  
514/12, 514/8

Full Title Citation Front Review Classification Date Reference Sequences Attachments

View Draw Desc Image

☐ 13. Document ID: US 6075119 A

L11: Entry 13 of 18

File: USPT

Jun 13, 2000

US-PAT-NO: 6075119

DOCUMENT-IDENTIFIER: US 6075119 A

**THIS PAGE BLANK (USPTO)**

TITLE: Peptides useful for reducing symptoms of toxic shock syndrome

DATE-ISSUED: June 13, 2000

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Bannan; Jason D.	Thompson Station	TN		
Zabriskie; John B.	New York	NY		

US-CL-CURRENT: 530/300; 424/130.1, 424/185.1, 424/192.1, 424/243.1, 424/244.1,  
530/324, 530/325, 530/326, 530/327, 530/328, 530/333, 530/350

Full	Title	Category	Print	Review	Classification	Date	Reference	Sequences	Attachments
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------

View	Draw	File	Image
------	------	------	-------

☐ 14. Document ID: US 5872233 A

L11: Entry 14 of 18

File: USPT

Feb 16, 1999

US-PAT-NO: 5872233

DOCUMENT-IDENTIFIER: US 5872233 A

TITLE: Mycoplasma arthritidis T-cell mitogen

DATE-ISSUED: February 16, 1999

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Cole; Barry C.	Sandy	UT		
Atkin; Curtis L.	Salt Lake City	UT		
Oliphant; Arnold R.	Johnston	IA		
Pole; Ann	Salt Lake City	UT		

US-CL-CURRENT: 536/23.7; 435/69.1, 436/86, 530/300, 530/324, 530/350, 536/22.1,  
536/23.1, 536/25.3

Full	Title	Category	Print	Review	Classification	Date	Reference	Sequences	Attachments
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------

View	Draw	File	Image
------	------	------	-------

☐ 15. Document ID: US 5795974 A

L11: Entry 15 of 18

File: USPT

Aug 18, 1998

US-PAT-NO: 5795974

DOCUMENT-IDENTIFIER: US 5795974 A

TITLE: Mycoplasma arthritidis superantigen

DATE-ISSUED: August 18, 1998

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Cole; Barry C.	Sandy	UT		
Atkin; Curtis L.	Holladay	UT		
Knudtson; Kevin L.	Salt Lake City	UT		

US-CL-CURRENT: 536/23.7; 435/5, 435/7.2

**THIS PAGE BLANK (USPTO)**

Full	Title	Category	Front	Review	Classification	Date	Reference	Sequences	Attachments
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------

MAC	Draw Data	Image
-----	-----------	-------

☐ 16. Document ID: US 5728388 A

L11: Entry 16 of 18

File: USPT

Mar 17, 1998

US-PAT-NO: 5728388

DOCUMENT-IDENTIFIER: US 5728388 A

TITLE: Method of cancer treatment

DATE-ISSUED: March 17, 1998

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Terman; David S.	Pebble Beach	CA	93953	

US-CL-CURRENT: 424/237.1; 424/236.1

Full	Title	Category	Front	Review	Classification	Date	Reference	Sequences	Attachments
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------

MAC	Draw Data	Image
-----	-----------	-------

☐ 17. Document ID: US 5639869 A

L11: Entry 17 of 18

File: USPT

Jun 17, 1997

US-PAT-NO: 5639869

DOCUMENT-IDENTIFIER: US 5639869 A

TITLE: Mycoplasma arthritidis T-cell mitogen

DATE-ISSUED: June 17, 1997

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Cole; Barry C.	Sandy	UT		
Atkin; Curtis L.	Salt Lake City	UT		
Oliphant; Arnold R.	Johnston	IA		
Pole; Ann	Salt Lake City	UT		

US-CL-CURRENT: 536/23.7; 424/264.1, 530/326, 530/350, 530/825

Full	Title	Category	Front	Review	Classification	Date	Reference	Sequences	Attachments
------	-------	----------	-------	--------	----------------	------	-----------	-----------	-------------

MAC	Draw Data	Image
-----	-----------	-------

☐ 18. Document ID: US 6447777 B1 WO 9736614 A1 AU 9724293 A

L11: Entry 18 of 18

File: DWPI

Sep 10, 2002

DERWENT-ACC-NO: 1997-549326

DERWENT-WEEK: 200263

COPYRIGHT 2003 DERWENT INFORMATION LTD

TITLE: Use of crosslinked Staphylococcal protein A - for treating auto-immune diseases, transplant rejection neoplastic diseases or infectious disease such as HIV infection

**THIS PAGE BLANK (USPTO)**



INVENTOR: REISER, R F; TERMAN, D S

PRIORITY-DATA: 1996US-024802P (March 29, 1996), 1997US-0828951 (March 28, 1997)

## PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
US 6447777 B1	September 10, 2002		000	A61K039/02
WO 9736614 A1	October 9, 1997	E	100	A61K039/09
AU 9724293 A	October 22, 1997		000	A61K039/09

INT-CL (IPC): A61 K 38/00; A61 K 39/02; A61 K 39/04; A61 K 39/085; A61 K 39/09; A61 K 45/00; A61 K 47/04; C07 K 1/00; C07 K 14/24; C07 K 14/315; C07 K 14/35; C07 K 17/02; C07 K 17/06; C07 K 17/14

Full Title Details Front Reem Classification Date Reference Sequence All keywords

1997 Title Date 1997

Generate Collection

Print

Term	Documents
PYROGENIC	7502
PYROGENICS	13
EXOTOXIN	4369
EXOTOXINS	847
(5 AND (PYROGENIC ADJ5 EXOTOXIN)). USPT,PGPB,JPAB,EPAB,DWPI,TDBD.	18
(L5 AND PYROGENIC ADJ5 EXOTOXIN). USPT,PGPB,JPAB,EPAB,DWPI,TDBD.	18

Display Format:

-

Change Format

[Previous Page](#)[Next Page](#)

**THIS PAGE BLANK (USPTO)**



PT diagnosis of superantigen-associated bacterial infections  
XX  
PS Example 12; Page 94-95; 18pp; English.  
XY

The present amino acid sequence of the Streptococcal pyrogenic exotoxin A (SPE-A), a bacterial superantigen toxin (SAg), used for the development of a DNA vaccine against streptococcal diseases, is altered by site directed mutagenesis at the coding region of this SAg toxin gene. The amino acid sequence of the mutant SAg toxin was confirmed by mass spectrometry. This mutant SAg toxin results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SPE-A has antibacterial and cytotoxic activity; this sequence is useful for the production of SPE-A vaccines against streptococcal infections. The characteristics of the chemically inactivated toxoids and its designed to be used as adjuvant against one or several related streptococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated bacterial infections.

**SQ Sequence 251 AA;**

Query Match	100.0%;	Score 1322;	DB 21;	Length 251;
Best Local Similarity	100.0%;	Pred NO. 4	5a-111;	

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0

[illegible]

RESULT 2  
APR70E09

ID ABB79508 standard; protein; 251 AA.

AC ABB79508;

DT 23-SEP-2002 (first entry)  
YY

Streptococcal pyrogenic exotoxin A vaccine SPEA42.

KW Exotoxin A; SPEa; SPEa42; superantigen; antigen; toxin; vaccine  
KW attenuation; mutant; muteln.

**Streptococcus pyogenes**

XX  
XX  
PN 1156309333-P104-JIN-2002  
PD  
XX

01-SEP-1998:

25-JUN-1997: 97US-0882431

PA (USSA ) US SEC OF ARMY.

PI Ulrich RG, Olson MA,

DR WPI; 2002-546281/58.

DR N-PSDB; ABN84229  
XY

**XX**      superantigen toxin-associated bacterial diseases -  
**PT**      Novel isolated and purified superantigen toxin DNA fragment which has  
**PR**      been genetically altered, useful for producing vaccine for treatment of  
**PX**

The prent sequence is the protein sequence of Streptococcus pyogenes vaccine SP942. The vaccine differs from the native SP94 sequence by substitution of the Leu-42 residue by Arg. This substitution is located in the non-antigenic region of the toxin and the HLA-DR receptor binding site of the toxin. SP94 contains a recombinant protein in *Escherichia coli* as a secreted protein or as a cytoplasmic product. No indicators of toxicity have been detected for the purified recombinant protein, and vaccine studies demonstrate that SP942 is highly antigenic, inducing protective immunity in a mouse animal model. The attenuated superantigen can be used as a model for the development of vaccines and for studies of protein processing and transport. The development of vaccines and therapy are provided by the invention. A multivalent vaccine consisting of altered superantigen toxins from SEB, SEB, SSC-1, TSSr-1 and SP94 is predicted to provide protective immunity against the majority of bacterial superantigen toxins.

**SD Sequence 251 AA**

Query Match	100.00;	Score 1322;	DB 23;	Length 251;
Best Local Similarity	100.00;	Pred NO. 4	5a-111;	

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	60	MMNNKVVYKAKMFFVFLVATFGLATLSQEFPAQDDPSDQJHSSSLVWMLNIFYEGSDP	60
Db	1	MMNNKVVYKAKMFFVFLVATFGLATLSQEFPAQDDPSDQJHSSSLVWMLNIFYELGSDP	60
Qy	61	THENKVSVDLSRSHDLTVNMSGFMDKAKTELKQDSMATLTKKKNDVIQGYEYHLCYC	120
Db	61	THENKVSVDLSRSHDLTVNMSGFMDKAKTELKQDSMATLTKKKNDVIQGYEYHLCYC	120
Qy	121	ENKRSASVYDGLNMGHSHLTPKATYKSTLQSGLSAPLTFENKATVMDQMDLYR	180
Db	121	ENKRSASVYDGLNMGHSHLTPKATYKSTLQSGLSAPLTFENKATVMDQMDLYR	180
Qy	181	KTLNDKRLQVYNGSPKRYETGYIKFIPKNSFSPDPPPEPFGSKTLVYIKNEDLSN	240
Db	181	KTLNDKRLQVYNGSPKRYETGYIKFIPKNSFSPDPPPEPFGSKTLVYIKNEDLSN	240
Qy	241	TSQIEVLYLTKR	251
Db	241	TSQIEVLYLTKR	251

**RESULT 3**

ID AAW12097 standard; Protein; 251 AA.

AC AAW12097

DT 04-NOV-1997 (first entry)

Streptococcus pyogenes Streptococcal toxin A

KM Streptococcal: toxin A; SPE-A; non-lethal; mutant; production;  
 KM vaccine: protection; treatment; cancer; neutralising antibody;  
 KM streptococcal toxic shock syndrome: STSS; symptom; amelioration;  
 KM fever: hypotension; group A streptococcal infection; myositis;  
 KM fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.  
 SS Streptococcus pyogenes.

	Key	Location/Qualifiers
EH	Peptide	1..30
FT		/label= sig_peptide
FT		

Peptide 31.251  
/Label=mat.peptide

WT 1997-099936/09.  
N-PSDB: AAM12091.

Ohlendorf D, Roggliani M, Schlievert PM, Stoeckert U.  
(MIND) UNIV MINNESOTA.

Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.

Disclosure: Pages 77-79; 102pp; English.

The present sequence is Streptococcus pyogenes Streptococcal toxin A (SPE-A), from which a non-lethal mutant SPE-A, compiling at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralizing STSS symptoms, e.g. CO be produced by hypotension group A streptococcal infection, myositis, fasciitis and liver damage. The neutralizing Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells.

Sequence 251 AA:

Query Match 98.9%; Score 1308; DB 18; Length 251;  
Best Local Similarity 99.2%; Pred. No. 8.3e-110;  
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MEMNKYKAKKVFPLVATFLGITSQVFAQDDPPSOLHRSLSVKNLONTFLYEDDPV 60  
1 MEMNKYKAKKVFPLVATFLGITSQVFAQDDPPSOLHRSLSVKNLONTFLYEDDPV 60

61 TERNKSVQDLSHLITVNSGPNYDKLTELKNDQMATLFDKNDVIGVETVHCLTC 120  
61 TERNKSVQDLSHLITVNSGPNYDKLTELKNDQMATLFDKNDVIGVETVHCLTC 120

121 ENNESACITGCVTGHGNSHLEIPKRIYVVSIDISQISLSDLETNNKWTVAQEDLYKVR 180  
121 ENNESACITGCVTGHGNSHLEIPKRIYVVSIDISQISLSDLETNNKWTVAQEDLYKVR 180

181 KYLDNKKQLYTNQSGKTEGKIFPKKKSSTNDFPPPEPFGSKITLMTYKNEFLDSN 240  
181 KYLDNKKQLYTNQSGKTEGKIFPKKKSSTNDFPPPEPFGSKITLMTYKNEFLDSN 240

241 TSOIEVLYLTK 251  
241 TSOIEVLYLTK 251

RESULT 4  
AAM59780 standard; Protein: 251 AA.  
AAM59780:  
12-OCT-1998 (first entry)

Amino acid sequence of Streptococcus pyogenes exotoxin A.  
SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;  
wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;  
streptococcal toxic shock syndrome; STSS; T cell lymphoma;  
uterine cancer.  
Streptococcus pyogenes.

WT 1997-099936/09.  
N-PSDB: AAM12091.

Ohlendorf D, Roggliani M, Schlievert PM, Stoeckert U.  
(MIND) UNIV MINNESOTA.

Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.

Disclosure: Pages 77-79; 102pp; English.

The present sequence is Streptococcus pyogenes Streptococcal toxin A (SPE-A), from which a non-lethal mutant SPE-A, compiling at least 1 amino acid change, can be derived. The mutant SPE-A can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralizing STSS symptoms, e.g. CO be produced by hypotension group A streptococcal infection, myositis, fasciitis and liver damage. The neutralizing Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells.

Sequence 251 AA:

Query Match 98.9%; Score 1308; DB 18; Length 251;  
Best Local Similarity 99.2%; Pred. No. 8.3e-110;  
Matches 249; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MEMNKYKAKKVFPLVATFLGITSQVFAQDDPPSOLHRSLSVKNLONTFLYEDDPV 60  
1 MEMNKYKAKKVFPLVATFLGITSQVFAQDDPPSOLHRSLSVKNLONTFLYEDDPV 60

61 TERNKSVQDLSHLITVNSGPNYDKLTELKNDQMATLFDKNDVIGVETVHCLTC 120  
61 TERNKSVQDLSHLITVNSGPNYDKLTELKNDQMATLFDKNDVIGVETVHCLTC 120

121 ENNESACITGCVTGHGNSHLEIPKRIYVVSIDISQISLSDLETNNKWTVAQEDLYKVR 180  
121 ENNESACITGCVTGHGNSHLEIPKRIYVVSIDISQISLSDLETNNKWTVAQEDLYKVR 180

181 KYLDNKKQLYTNQSGKTEGKIFPKKKSSTNDFPPPEPFGSKITLMTYKNEFLDSN 240  
181 KYLDNKKQLYTNQSGKTEGKIFPKKKSSTNDFPPPEPFGSKITLMTYKNEFLDSN 240

241 TSOIEVLYLTK 251  
241 TSOIEVLYLTK 251

RESULT 5  
AAM12154 standard; Protein: 251 AA.  
AAM12154:  
12-OCT-1998 (first entry)

AC AAM12146;  
 XX 04-NOV-1997 (first entry)  
 XX Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.  
 DE Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;  
 XX vaccine; protection; treatment; cancer; neutralising antibody;  
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;  
 KM fasciitis; liver damage; group A streptococcal infection; myositis;  
 XX fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.  
 OS Streptococcus pyogenes.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 XX Peptide 1..30  
 XX /label= sig\_peptide  
 XX Peptide 31..251  
 XX /label= mat\_peptide  
 XX Misc-difference 225  
 XX /note= "wild type Ser replaced by Ala"  
 XX MO6640930-A1.  
 XX PD 19-DEC-1996.  
 XX 07-JUN-1996; 96MO-US10252.  
 XX 07-JUN-1995; 95US-0480261.  
 XX (MINN ) UNIV MINNESOTA.  
 XX Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;  
 WPI: 1997-099936/09.  
 XX Mutant SPE-A toxin with at least one amino acid change is  
 XX substantially non-lethal - used in vaccine composition for  
 XX treatment of cancer and streptococcal toxic shock syndrome etc.  
 XX Example 4: Page -; 102pp: English.  
 XX The present sequence is a non-lethal Streptococcus pyogenes  
 XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce  
 XX vaccines to protect animals against wild type SPE-A and to treat  
 XX cancer and streptococcal toxic shock syndrome (STSS). The mutant  
 XX SPE-A causes neutralising antibodies (Ab) to be produced, which  
 XX can be used to ameliorate STSS symptoms, e.g. fever, hypotension,  
 XX group A streptococcal infection, myositis, fasciitis and liver  
 XX damage. The neutralising Ab is preferably administered in  
 XX conjunction with antibiotic therapy. The mutant SPE-A is  
 XX especially useful for treating T cell lymphomas, and ovarian and  
 XX uterine cancer. It is thought that mutant SPE-A can be selectively  
 XX used against T cell lymphoma cells.  
 XX N.B. Sequence not given in the specification, but constructed  
 XX using the wild type SPE-A sequence given on pages 77-79.  
 XX Sequence 251 AA:  
 Query Match 98.7%; Score 1305; DB 18; Length 251;  
 Best Local Similarity 98.8%; Pred. No. 1.5e-109;  
 Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 0Y 1 MNNKKYKKKFFVYVTEGLTISGVPAQDPSPQSHRSSTLVKNLONTIPLYESDPV 60  
 1 MNNKKYKKKFFVYVTEGLTISGVPAQDPSPQSHRSSTLVKNLONTIPLYESDPV 60  
 DB 1 MNNKKYKKKFFVYVTEGLTISGVPAQDPSPQSHRSSTLVKNLONTIPLYESDPV 60  
 0Y 1 MNNKKYKKKFFVYVTEGLTISGVPAQDPSPQSHRSSTLVKNLONTIPLYESDPV 60  
 61 THNNKSVQQLSHSDIYNNSPPYKTKTEKLNQEMALTEKKNKWDITGVYHYHLCYC 120  
 DB 61 THNNKSVQQLSHSDIYNNSPPYKTKTEKLNQEMALTEKKNKWDITGVYHYHLCYC 120  
 0Y 121 ENAKRSACITGCTGTNHCNHLERFKATIVYVSDTIGTSLSDIETNKKWATQELDYKVA 180

DB 121 ENAKRSACITGCTGTNHCNHLERFKATIVYVSDTIGTSLSDIETNKKWATQELDYKVA 180  
 0Y 181 KTLRDNKQLTNTGNSKRYETGKIFPRNKSPPFPPFPTOSTLTLATYKQNTLDSN 240  
 DB 181 KTLRDNKQLTNTGNSKRYETGKIFPRNKSPPFPPFPTOSTLTLATYKQNTLDSN 240  
 0Y 241 TSOILEVYLTNR 251  
 DB 241 TSOILEVYLTNR 251  
 RESULT 6  
 AAM12146  
 XX AAM12146 standard; Protein; 251 AA.  
 XX AAM12146;  
 XX 04-NOV-1997 (first entry)  
 XX Streptococcus pyogenes Streptococcal toxin A mutant Lys197Glu.  
 DE Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;  
 XX vaccine; protection; treatment; cancer; neutralising antibody;  
 KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;  
 KM fever; hypotension; group A streptococcal infection; myositis;  
 XX fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.  
 OS Streptococcus pyogenes.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 XX Peptide 1..30  
 XX /label= sig\_peptide  
 XX Peptide 31..251  
 XX /label= mat\_peptide  
 XX Misc-difference 180  
 XX /note= "wild type Lys replaced by Glu"  
 XX MO6640930-A1.  
 XX PD 19-DEC-1996.  
 XX 07-JUN-1996; 96MO-US10252.  
 XX 07-JUN-1995; 95US-0480261.  
 XX (MINN ) UNIV MINNESOTA.  
 XX Ohlendorf D, Roggiani M, Schlievert PM, Stoehr J;  
 WPI: 1997-099936/09.  
 XX Mutant SPE-A toxin with at least one amino acid change is  
 XX substantially non-lethal - used in vaccine composition for  
 XX treatment of cancer and streptococcal toxic shock syndrome etc.  
 XX Example 5: Page -; 102pp: English.  
 XX The present sequence is a non-lethal Streptococcus pyogenes  
 XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce  
 XX vaccines to protect animals against wild type SPE-A and to treat  
 XX cancer and streptococcal toxic shock syndrome (STSS). The mutant  
 XX SPE-A causes neutralising antibodies (Ab) to be produced, which  
 XX can be used to ameliorate STSS symptoms, e.g. fever, hypotension,  
 XX group A streptococcal infection, myositis, fasciitis and liver  
 XX damage. The neutralising Ab is preferably administered in  
 XX conjunction with antibiotic therapy. The mutant SPE-A is  
 XX especially useful for treating T cell lymphomas, and ovarian and  
 XX uterine cancer. It is thought that mutant SPE-A can be selectively  
 XX used against T cell lymphoma cells.  
 XX N.B. Sequence not given in the specification, but constructed  
 XX using the wild type SPE-A sequence given on pages 77-79.

```

XX Sequence 251 AA:
SQ
Query Match
Best Local Similarity 98.84; Score 1304; DB 18; Length 251;
Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MENNKKVLRKMFVLTFTGLTISQVFAQDDPDSQLRSSLVNNKQNTYELTEDBV 60
DB 1 MENNKKVLRKMFVLTFTGLTISQVFAQDDPDSQLRSSLVNNKQNTYELTEDBV 60
OY 61 THEMVSVDQLSSDILTVNVSQPNYDKATTELKNOBANTLFRKNDVIGVEYHLCYLC 120
DB 61 THEMVSVDQLSSDILTVNVSQPNYDKATTELKNOBANTLFRKNDVIGVEYHLCYLC 120
OY 121 ENAERSACIYGVTNHEGSHLETPKRIYKVSIDGJSLSPDITFNKKKWTAGLELDYKVR 180
DB 121 ENAERSACIYGVTNHEGSHLETPKRIYKVSIDGJSLSPDITFNKKKWTAGLELDYKVR 180
OY 181 KYLDNRKQLYTNGSKYETGYIKETIPKNESEFMPDFPEPEPTOSKYLMIYKONETLDSN 240
DB 181 KYLDNRKQLYTNGSKYETGYIKETIPKNESEFMPDFPEPEPTOSKYLMIYKONETLDSN 240

OY 241 TSOIEVYLTTR 251
DB 241 TSOIEVYLTTR 251

RESULT 7
AA12150 standard; Protein: 251 AA.
AA12150:
04-NOV-1997 (first entry)
DE Streptococcus pyogenes Streptococcal toxin A mutant Lys16Asn.
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KW vaccine; protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KW fever; hypotension; group A streptococcal infection; myositis;
KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT 1 1absl- sig-peptide
FT 2 1absl- sig
FT 3 1absl- mat-peptide
FT Misc-difference 46
FT /note= "wild type lys replaced by Asp"
XX
XX MO9640930-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96MO-US1052.
XX
XX 07-JUN-1995; 95US-0480261.
XX
XX (MIND ) UNIV MINNESOTA.
XX
XX Ohlendorf D, Roggiani M, Schliwert PM, Stoen J;
XX
XX WPI. 1997-09936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is
XX substantially non-lethal - used in vaccine composition for
XX treatment of cancer and streptococcal toxic shock syndrome etc.
XX

```

```

PS Example 4; Page -: 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes
CC Streptococcal toxin A (SPE-A) mutant, which can be used to produce
CC vaccine for protection against streptococcal toxic shock syndrome (TSS) and to treat
CC cancer and streptococcal toxic shock syndrome (STSS). The mutant
CC SPE-A causes neutralising antibodies (Ab) to be produced, which
CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,
CC group A streptococcal infection, myositis, fasciitis and liver
CC damage. The neutralising Ab is preferably administered in
CC conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphoma, and ovarian and
CC uterine cancer. It is suggested that mutant SPE-A can be selectively
CC toxic to T cell lymphoma cells.
CC N.B. Sequence not given in the specification, but constructed
CC using the wild type SPE-A sequence given on pages 77-79.
XX
XX Sequence .251 AA:
SQ
Query Match
Best Local Similarity 98.84; Score 1303; DB 18; Length 251;
Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MENNKKVLRKMFVLTFTGLTISQVFAQDDPDSQLRSSLVNNKQNTYELTEDBV 60
DB 1 MENNKKVLRKMFVLTFTGLTISQVFAQDDPDSQLRSSLVNNKQNTYELTEDBV 60
OY 61 THEMVSVDQLSSDILTVNVSQPNYDKATTELKNOBANTLFRKNDVIGVEYHLCYLC 120
DB 61 THEMVSVDQLSSDILTVNVSQPNYDKATTELKNOBANTLFRKNDVIGVEYHLCYLC 120
OY 121 ENAERSACIYGVTNHEGSHLETPKRIYKVSIDGJSLSPDITFNKKKWTAGLELDYKVR 180
DB 121 ENAERSACIYGVTNHEGSHLETPKRIYKVSIDGJSLSPDITFNKKKWTAGLELDYKVR 180
OY 181 KYLDNRKQLYTNGSKYETGYIKETIPKNESEFMPDFPEPEPTOSKYLMIYKONETLDSN 240
DB 181 KYLDNRKQLYTNGSKYETGYIKETIPKNESEFMPDFPEPEPTOSKYLMIYKONETLDSN 240

OY 241 TSOIEVYLTTR 251
DB 241 TSOIEVYLTTR 251

RESULT 8
AA12147 standard; Protein: 251 AA.
AA12147:
04-NOV-1997 (first entry)
DE Streptococcus pyogenes Streptococcal toxin A mutant Asn20Asp.
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;
KW vaccine; protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration;
KW fever; hypotension; group A streptococcal infection; myositis;
KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT 1 1absl- sig-peptide
FT 2 1absl- sig
FT 3 1absl- mat-peptide
FT Misc-difference 50
FT /note= "wild type Asn replaced by Asp"
XX
XX MO9640930-A1.
XX

```

PD 19-DEC-1996.  
 XX 07-JUN-1996; 96NO-US10352.  
 PF 07-JUN-1995; 95US-0460261.  
 XX (MNU ) UNIV MINNESOTA.  
 PA Ohlendorf D, Roginski M, Schlievert PM, Stoehr J;  
 PI WPI: 1997-099936/09.  
 DR Mutant SPE-A toxin with at least one amino acid change is  
 XX substantially non-lethal - used in vaccine composition for  
 PT treatment of cancer and streptococcal toxic shock syndrome etc.  
 XX  
 PS Claim 5; Page -: 102pp; English.  
 CC The present sequence is a non-lethal Streptococcus pyogenes  
 CC streptococcal toxin A (SPE-A) mutant, which can be used to produce  
 CC vaccines to protect animals against wild type SPE-A and to treat  
 CC cancer and streptococcal toxic shock syndrome (STSS). The  
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which  
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,  
 CC group A streptococcal infection, myositis, fasciitis and liver  
 CC damage. The neutralising Ab is preferably administered in  
 CC conjunction with antibiotic therapy. The mutant SPE-A is  
 CC especially useful for treating T cell lymphomas and ovarian and  
 CC uterine cancer. It is thought that mutant SPE-A can be selectively  
 CC toxic to T cell lymphoma cells  
 CC N.B. Sequence not given in the specification, but constructed  
 CC using the wild type SPE-A sequence given on pages 77-79.  
 XX  
 SQ Sequence 251 AA:

Query Match 98.6%; Score 1303; DB 18; Length 251;  
 Best Local Similarity 98.8%; Pred. No. 2, 3e-109;  
 Matches 248; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

0Y 1 MENNKKYLLKRWFFVLYTFGLTISQVPAQDPSPQSOLHSSIVKNIQNIIFYLESDPV 60  
 DB 1 MENNKKYLLKRWFFVLYTFGLTISQVPAQDPSPQSOLHSSIVKNIQNIIFYLESDPV 60  
 0Y 61 THENKSVQDLKSHDIYVNSQPPYKRLKTELKNQDMATLKKONANDIVGYEYHLCYC 120  
 DB 61 THENKSVQDLKSHDIYVNSQPPYKRLKTELKNQDMATLKKONANDIVGYEYHLCYC 120  
 0Y 61 THENKSVQDLKSHDIYVNSQPPYKRLKTELKNQDMATLKKONANDIVGYEYHLCYC 120  
 DB 121 ENNERSACTIGCVTNHESNHLKPKIKYKVSIDIOSLSFDLETKNKMTNOBOLDYVR 180  
 0Y 121 ENNERSACTIGCVTNHESNHLKPKIKYKVSIDIOSLSFDLETKNKMTNOBOLDYVR 180  
 DB 121 ENNERSACTIGCVTNHESNHLKPKIKYKVSIDIOSLSFDLETKNKMTNOBOLDYVR 180  
 0Y 181 KYLTNNQOLYTNKSPKSEYETGYIKFKPKNKSEFPDFPPEFQSKYLYIMDNDETLDSN 240  
 DB 181 KYLTNNQOLYTNKSPKSEYETGYIKFKPKNKSEFPDFPPEFQSKYLYIMDNDETLDSN 240  
 0Y 241 TSGIENVLTK 251  
 DB 241 TSGIENVLTK 251  
 DB  
 RESULT 9  
 AAM12148 standard; Protein; 251 AA.  
 AAM12148;  
 04-NOV-1997 (first entry)  
 XX Streptococcus pyogenes Streptococcal toxin A mutant N20D/K157E.  
 XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;  
 XX vaccine; protection; treatment; cancer; neutralising antibody;  
 XX streptococcal toxic shock syndrome; STSS; symptom; amelioration;

KW fever; hypotension; group A streptococcal infection; myositis;  
 KW fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.  
 XX Streptococcus pyogenes.  
 OS Synthetic.  
 XX  
 XX Key location/Qualifiers  
 XX Peptide /label= sig-peptide  
 XX Peptide 31..251  
 XX /label= mat-peptide  
 FT Misc-difference 50  
 FT /note= "wild type Asn replaced by Asp"  
 FT Misc-difference 187  
 FT /note= "wild type Lys replaced by Glu"  
 XX  
 XX W06940930-A1.  
 XX  
 PD 19-DEC-1996.  
 XX 07-JUN-1996; 96NO-US10352.  
 PF 07-JUN-1995; 95US-0460261.  
 XX (MNU ) UNIV MINNESOTA.  
 PA Ohlendorf D, Roginski M, Schlievert PM, Stoehr J;  
 PI WPI: 1997-099936/09.  
 DR Mutant SPE-A toxin with at least one amino acid change is  
 XX substantially non-lethal - used in vaccine composition for  
 PT treatment of cancer and streptococcal toxic shock syndrome etc.  
 XX  
 PS Claim 5; Page -: 102pp; English.  
 CC The present sequence is a non-lethal Streptococcus pyogenes  
 CC streptococcal toxin A (SPE-A) mutant, which can be used to produce  
 CC vaccines to protect animals against wild type SPE-A and to treat  
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant  
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which  
 CC may be used to ameliorate STSS symptoms, e.g. fever, hypotension,  
 CC group A streptococcal infection, myositis, fasciitis and liver  
 CC damage. The neutralising Ab is preferably administered in  
 CC conjunction with antibiotic therapy. The mutant SPE-A is  
 CC especially useful for treating T cell lymphomas and ovarian and  
 CC uterine cancer. It is thought that mutant SPE-A can be selectively  
 CC toxic to T cell lymphoma cells.  
 CC N.B. Sequence not given in the specification, but constructed  
 CC using the wild type SPE-A sequence given on pages 77-79.  
 XX  
 SQ Sequence 251 AA:

Query Match 98.3%; Score 1299; DB 18; Length 251;  
 Best Local Similarity 98.4%; Pred. No. 5, 4e-109;  
 Matches 247; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

0Y 1 MENNKKYLLKRWFFVLYTFGLTISQVPAQDPSPQSOLHSSIVKNIQNIIFYLESDPV 60  
 DB 1 MENNKKYLLKRWFFVLYTFGLTISQVPAQDPSPQSOLHSSIVKNIQNIIFYLESDPV 60  
 0Y 61 THENKSVQDLKSHDIYVNSQPPYKRLKTELKNQDMATLKKONANDIVGYEYHLCYC 120  
 DB 61 THENKSVQDLKSHDIYVNSQPPYKRLKTELKNQDMATLKKONANDIVGYEYHLCYC 120  
 0Y 61 THENKSVQDLKSHDIYVNSQPPYKRLKTELKNQDMATLKKONANDIVGYEYHLCYC 120  
 DB 121 ENNERSACTIGCVTNHESNHLKPKIKYKVSIDIOSLSFDLETKNKMTNOBOLDYVR 180  
 0Y 121 ENNERSACTIGCVTNHESNHLKPKIKYKVSIDIOSLSFDLETKNKMTNOBOLDYVR 180  
 DB 121 ENNERSACTIGCVTNHESNHLKPKIKYKVSIDIOSLSFDLETKNKMTNOBOLDYVR 180  
 0Y 181 KYLTNNQOLYTNKSPKSEYETGYIKFKPKNKSEFPDFPPEFQSKYLYIMDNDETLDSN 240  
 DB 181 KYLTNNQOLYTNKSPKSEYETGYIKFKPKNKSEFPDFPPEFQSKYLYIMDNDETLDSN 240



QY 241 TSOIEVLYTRK 251  
 DB 241 TSOIEVLYTRK 251

## RESULT 10

AA12151 ID AAM12151 standard; Protein: 251 AA.

AA12151:

04-NOV-1997 (first entry)

Streptococcus pyogenes Streptococcal toxin A mutant Cys87Ser.  
 Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;  
 vaccine; protection; treatment; cancer; neutralising antibody;  
 streptococcal toxic shock syndrome; STSS; symptom; amelioration;  
 fever; hypotension; group A streptococcal infection; myositis;  
 fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.  
 Streptococcus pyogenes.  
 Synthetic.

Key Location/Qualifiers  
 Peptide 1..30  
 Peptide /label= sig\_peptide  
 Peptide 31..251  
 Peptide /label= mat\_peptide  
 Misc-difference 117  
 /note= "wild type Cys replaced by Ser"

MO9640930-A1.

19-DEC-1996.

07-JUN-1996: 96MO-US10252.

07-JUN-1995: 95US-0480261.

(MINU) UNIV MINNESOTA.

Ohlendorf D, Roggliani M, Schlevert PM, Steehr J;

WPI: 1997-09936/09.

Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.  
 Example 4; Page -: 102pp; English.

The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat animals with streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibody (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fasciitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and testicular cancer. It is thought that mutant SPE-A can be selectively toxic to T cells. The mutant SPE-A can be used in a vaccine to treat N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79.

Sequence 251 AA:

Query Match 98.2%; Score 1298; DB 18; Length 251;  
 Background Similarity 98.8%; Pred. No. 6,6e-109;  
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MEHKKVLAHVFVLYTFGLTISQVFAQODPPQSQRSLRYNKNQNYFLYECDDY 60  
 DB 1 MEHKKVLAHVFVLYTFGLTISQVFAQODPPQSQRSLRYNKNQNYFLYECDDY 60  
 QY 61 THENYKSVQDLSHDLITNVSQPNIDKLTELNDQANLFDKNDIVGEVYHLCYIC 120  
 DB 61 THENYKSVQDLSHDLITNVSQPNIDKLTELNDQANLFDKNDIVGEVYHLCYIC 120  
 QY 121 ENMRSACTYGGVYNEHGNHLETPKLYVKSIDIGSLSPDIEYTKKMYTQDELKYKR 180  
 DB 121 ENMRSACTYGGVYNEHGNHLETPKLYVKSIDIGSLSPDIEYTKKMYTQDELKYKR 180  
 QY 181 KILDNKLITNGSKSTGYTIFIPNNESFNPDPFPEPTQSKYTLTYMDNETLDSN 240  
 DB 181 KILDNKLITNGSKSTGYTIFIPNNESFNPDPFPEPTQSKYTLTYMDNETLDSN 240

## RESULT 11

AA12152 ID AAM12152 standard; Protein: 251 AA.

AA12152:

04-NOV-1997 (first entry)

Streptococcus pyogenes Streptococcal toxin A mutant Cys98Ser.  
 Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;  
 vaccine; protection; treatment; cancer; neutralising antibody;  
 streptococcal toxic shock syndrome; STSS; symptom; amelioration;  
 fever; hypotension; group A streptococcal infection; myositis;  
 fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.  
 Streptococcus pyogenes.  
 Synthetic.

Key Location/Qualifiers  
 Peptide 1..30  
 Peptide /label= sig\_peptide  
 Peptide 31..251  
 Peptide /label= mat\_peptide  
 Misc-difference 128  
 /note= "wild type Cys replaced by Ser"

MO9640930-A1.

19-DEC-1996.

07-JUN-1996: 96MO-US10252.

07-JUN-1995: 95US-0480261.

(MINU) UNIV MINNESOTA.

Ohlendorf D, Roggliani M, Schlevert PM, Steehr J;

WPI: 1997-09936/09.

Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.  
 Example 4; Page -: 102pp; English.

The present sequence is a non-lethal Streptococcus pyogenes Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat animals with streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced. The mutant

CC may be used to ameliorate STSS symptoms, e.g., fever, hypotension,  
 CC group A streptococcal infection, myositis, fasciitis and liver  
 CC damage. The neutralising Ab is preferably administered in  
 CC conjunction with antibiotic therapy. The mutant SPE-A is  
 CC especially useful for treating T cell lymphomas, and ovarian and  
 CC uterine cancer. It is thought that mutant SPE-A can be selectively  
 CC toxic to T cell lymphoma cells.  
 CC N.B. Sequence not given in the specification, but constructed  
 CC using the wild type SPE-A sequence given on pages 77-79.  
 XX

Sequence 251 AA:  
 Query Match 98.2%; Score 1298; DB 18; Length 251;  
 Best Local Similarity 98.8%; Pred. No. 6,6e-109;  
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 1 MENNKKVYAKKMFVLYTFGLGTLTISQVFAQDDPPSQILHSSLYVKNQNTFYLYECSDPV 60  
 1 MENNKKVYAKKMFVLYTFGLGTLTISQVFAQDDPPSQILHSSLYVKNQNTFYLYECSDPV 60  
 61 THENKSVYDQLSHDLIYVSGPNYDKLTFLKNOEMATLFFDKMNDIVGVEYHLCYLS 120  
 61 THENKSVYDQLSHDLIYVSGPNYDKLTFLKNOEMATLFFDKMNDIVGVEYHLCYLS 120  
 61 THENKSVYDQLSHDLIYVSGPNYDKLTFLKNOEMATLFFDKMNDIVGVEYHLCYLS 120  
 61 THENKSVYDQLSHDLIYVSGPNYDKLTFLKNOEMATLFFDKMNDIVGVEYHLCYLS 120  
 121 ENKESACITGCVTNHESNHLIEIPKIKVYKSIDTOSLSPDIEFNKMYTAQELDYKVR 180  
 121 ENKESACITGCVTNHESNHLIEIPKIKVYKSIDTOSLSPDIEFNKMYTAQELDYKVR 180  
 121 ENKESACITGCVTNHESNHLIEIPKIKVYKSIDTOSLSPDIEFNKMYTAQELDYKVR 180  
 121 ENKESACITGCVTNHESNHLIEIPKIKVYKSIDTOSLSPDIEFNKMYTAQELDYKVR 180  
 181 KYLTNMQLYTNGSPSKYETGYIKFIPKKNSEFMPFPPEPTOSKYLIMYDKNETLDSN 240  
 181 KYLTNMQLYTNGSPSKYETGYIKFIPKKNSEFMPFPPEPTOSKYLIMYDKNETLDSN 240  
 181 KYLTNMQLYTNGSPSKYETGYIKFIPKKNSEFMPFPPEPTOSKYLIMYDKNETLDSN 240  
 181 KYLTNMQLYTNGSPSKYETGYIKFIPKKNSEFMPFPPEPTOSKYLIMYDKNETLDSN 240  
 241 TSOILEVLYTKR 251  
 241 TSOILEVLYTKR 251

DB 241 TSOILEVLYTKR 251  
 241 TSOILEVLYTKR 251

RESULT 12  
 AAM12153 standard; Protein; 251 AA.  
 ID AAM12153;  
 XX 04-NOV-1997 (first entry)  
 XX Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.  
 DE Streptococcal toxin A; SPE-A; non-lethal; mutant; production;  
 KM streptococcal toxic shock syndrome; neutralising antibody;  
 KM streptococcal toxic shock syndrome STSS; symptom amelioration;  
 KM fever; hypotension; group A streptococcal infection; myositis;  
 KM fasciitis; liver damage; T cell lymphoma; ovarian; uterine.  
 XX

OS Streptococcus pyogenes.  
 XX Synthetic.  
 XX Key location/Qualifiers  
 XX Peptide 1 30  
 XX /label- sig\_peptide  
 FT Peptide 31..251  
 FT /label- mat\_peptide  
 FT Misc-difference 120  
 FT /note- "wild type Cys replaced by Ser"  
 XX W06640930-A1.  
 XX 19-DEC-1996.  
 PD 07-JUN-1996; 96MD-US10252.  
 XX 07-JUN-1995; 95US-0480261.  
 XX (MIMD ) UNIV MINNESOTA.  
 XX ZA

XX Ohlendorf D, Roggiani M, Schlievert PW, Stoehr J;  
 XX WPI; 1997-099936/09.  
 DR Mutant SPE-A toxin with at least one amino acid change is  
 XX substantially non-lethal - used in vaccine composition for  
 PT treatment of cancer and streptococcal toxic shock syndrome etc.  
 XX

PS Example 4; Page -; 102pp; English.  
 XX

CC The present sequence is a non-lethal Streptococcus pyogenes  
 CC vaccine to protect animals against wild type SPE-A and to treat  
 CC cancer and streptococcal toxic shock syndrome (STSS). The mutant  
 CC SPE-A causes neutralising antibodies (Ab) to be produced, which  
 CC may be used to ameliorate STSS symptoms, e.g., fever, hypotension,  
 CC group A streptococcal infection, myositis, fasciitis and liver  
 CC damage. The neutralising Ab is preferably administered in  
 CC conjunction with antibiotic therapy. The mutant SPE-A is  
 CC especially useful for treating T cell lymphomas and ovarian and  
 CC uterine cancer. It is thought that mutant SPE-A can be selectively  
 CC toxic to T cell lymphoma cells.  
 CC N.B. Sequence not given in the specification, but constructed  
 CC using the wild type SPE-A sequence given on pages 77-79.  
 XX

Sequence 251 AA:  
 Query Match 98.2%; Score 1298; DB 18; Length 251;  
 Best Local Similarity 98.8%; Pred. No. 6,6e-109;  
 Matches 248; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 1 MENNKKVYAKKMFVLYTFGLGTLTISQVFAQDDPPSQILHSSLYVKNQNTFYLYECSDPV 60  
 1 MENNKKVYAKKMFVLYTFGLGTLTISQVFAQDDPPSQILHSSLYVKNQNTFYLYECSDPV 60  
 1 MENNKKVYAKKMFVLYTFGLGTLTISQVFAQDDPPSQILHSSLYVKNQNTFYLYECSDPV 60  
 1 MENNKKVYAKKMFVLYTFGLGTLTISQVFAQDDPPSQILHSSLYVKNQNTFYLYECSDPV 60  
 61 THENKSVYDQLSHDLIYVSGPNYDKLTFLKNOEMATLFFDKMNDIVGVEYHLCYLS 120  
 61 THENKSVYDQLSHDLIYVSGPNYDKLTFLKNOEMATLFFDKMNDIVGVEYHLCYLS 120  
 61 THENKSVYDQLSHDLIYVSGPNYDKLTFLKNOEMATLFFDKMNDIVGVEYHLCYLS 120  
 61 THENKSVYDQLSHDLIYVSGPNYDKLTFLKNOEMATLFFDKMNDIVGVEYHLCYLS 120  
 121 ENKESACITGCVTNHESNHLIEIPKIKVYKSIDTOSLSPDIEFNKMYTAQELDYKVR 180  
 121 ENKESACITGCVTNHESNHLIEIPKIKVYKSIDTOSLSPDIEFNKMYTAQELDYKVR 180  
 121 ENKESACITGCVTNHESNHLIEIPKIKVYKSIDTOSLSPDIEFNKMYTAQELDYKVR 180  
 121 ENKESACITGCVTNHESNHLIEIPKIKVYKSIDTOSLSPDIEFNKMYTAQELDYKVR 180  
 181 KYLTNMQLYTNGSPSKYETGYIKFIPKKNSEFMPFPPEPTOSKYLIMYDKNETLDSN 240  
 181 KYLTNMQLYTNGSPSKYETGYIKFIPKKNSEFMPFPPEPTOSKYLIMYDKNETLDSN 240  
 181 KYLTNMQLYTNGSPSKYETGYIKFIPKKNSEFMPFPPEPTOSKYLIMYDKNETLDSN 240  
 181 KYLTNMQLYTNGSPSKYETGYIKFIPKKNSEFMPFPPEPTOSKYLIMYDKNETLDSN 240  
 241 TSOILEVLYTKR 251  
 241 TSOILEVLYTKR 251

DB 241 TSOILEVLYTKR 251  
 241 TSOILEVLYTKR 251

RESULT 13  
 AAM12149 standard; Protein; 251 AA.  
 ID AAM12149;  
 XX 04-NOV-1997 (first entry)  
 XX Streptococcus pyogenes Streptococcal toxin A mutant N20D/C38S.  
 DE Streptococcal toxin A; SPE-A; non-lethal; mutant; production;  
 KM streptococcal toxic shock syndrome; neutralising antibody;  
 KM streptococcal toxic shock syndrome STSS; symptom amelioration;  
 KM fever; hypotension; group A streptococcal infection; myositis;  
 KM fasciitis; liver damage; T cell lymphoma; ovarian; uterine.  
 XX

OS Streptococcus pyogenes.  
 XX Synthetic.  
 XX Key location/Qualifiers  
 XX Peptide 1 30  
 XX /label- sig\_peptide  
 FT Peptide 31..251  
 FT /label- mat\_peptide  
 FT Misc-difference 120  
 FT /note- "wild type Cys replaced by Ser"  
 XX W06640930-A1.  
 XX 19-DEC-1996.  
 PD 07-JUN-1996; 96MD-US10252.  
 XX 07-JUN-1995; 95US-0480261.  
 XX (MIMD ) UNIV MINNESOTA.  
 XX ZA

FT Peptide 1..30  
 FT /label= sig\_peptide  
 FT 31..251  
 FT /label= mat\_peptide  
 FT Misc-difference 50  
 FT /note= "wild type Asn replaced by Asp"  
 FT Misc-difference 128  
 FT /note= "wild type Cys replaced by Ser"  
 XX  
 XX MO6640930-A1.  
 XX  
 XX 19-DEC-1996.  
 XX  
 XX 07-JUN-1996; 96MO-US10252.  
 XX  
 XX 07-JUN-1995; 95US-0480261.  
 XX  
 XX (MIND ) UNIV MINNESOTA.  
 XX  
 XX Ohlendorf D, Roggliani M, Schlievert PM, Stoeck J;  
 XX WPI: 1997-099936/09.  
 XX  
 XX Mutant SPE-A toxin with at least one amino acid change is  
 XX substantially non-lethal - used in vaccine composition for  
 XX treatment of cancer and streptococcal toxic shock syndrome etc.  
 XX  
 XX Claim 5; Page -: 102pp; English.  
 XX  
 XX The present sequence is a non-lethal Streptococcus pyogenes  
 XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce  
 XX vaccines to protect animals against wild type SPE-A and to treat  
 XX cancer and streptococcal toxic shock syndrome (STSS). The mutant  
 XX SPE-A causes neutralising antibodies (Ab) to be produced, which  
 XX may be used to ameliorate STSS symptoms, e.g. fever, hypotension,  
 XX multiple organ dysfunction, and liver and kidney damage.  
 XX damage. The neutralising Ab is preferably administered in  
 XX conjunction with antibiotic therapy. The mutant SPE-A is  
 XX especially useful for treating T cell lymphomas, and ovarian and  
 XX uterine cancer. It is thought that mutant SPE-A can be selectively  
 XX toxic to T cell lymphoma cells.  
 XX N.B. Sequence not given in the specification, but constructed  
 XX using the wild type SPE-A sequence given on pages 77-79.  
 XX  
 XX Sequence 251 AA:  
 XX  
 XX Query Match 97.8%; Score 1293; DB 18; Length 251;  
 XX Best Local Similarity 98.4%; Pred. No. 1.9e-108;  
 XX Matches 247; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 XX  
 XX 1 MNNKKYKLVKMFVYVTEGLTISQVFAQDDPPDSQHRSSLVKMNQITFLYEGCPY 60  
 XX DB 1 MNNKKYKLVKMFVYVTEGLTISQVFAQDDPPDSQHRSSLVKMNQITFLYEGCPY 60  
 XX  
 XX 61 TERNKSVQDLSSHLLIYNVSPYVYKLTKEKNQENAKLTKRKNAVDTGVEYHLCYL 120  
 XX DB 61 TERNKSVQDLSSHLLIYNVSPYVYKLTKEKNQENAKLTKRKNAVDTGVEYHLCYL 120  
 XX  
 XX 121 ENAKRSACITGVYTHNBSNHLIFPKATVYVVISDIOISLDFETNNKAVYAOGLDYVR 180  
 XX DB 121 ENAKRSACITGVYTHNBSNHLIFPKATVYVVISDIOISLDFETNNKAVYAOGLDYVR 180  
 XX  
 XX 161 KYLDNNKQLYTNGPSEKTEGTYLTKFKKNSCFEPDPPEPFQSKALMTYNDNETLSN 240  
 XX DB 161 KYLDNNKQLYTNGPSEKTEGTYLTKFKKNSCFEPDPPEPFQSKALMTYNDNETLSN 240  
 XX  
 XX 241 TSGIETVLTTR 251  
 XX DB 241 TSGIETVLTTR 251  
 XX  
 XX 241 TSGIETVLTTR 251  
 XX DB 241 TSGIETVLTTR 251

ID AAM12145 standard; Protein; 250 AA.  
 XX AAM12145:  
 XX 04-NOV-1997 (first entry)  
 XX  
 XX Streptococcus pyogenes Streptococcal toxin A mutant delta88.  
 XX  
 XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;  
 XX vaccine; protection; treatment; cancer; neutralising antibody;  
 XX streptococcal toxic shock syndrome; STSS; symptom; amelioration;  
 XX hypotension; fever; liver damage; T cell; lymphoma; ovarian; uterine;  
 XX fascitis; liver damage; T cell; lymphoma; ovarian; uterine.  
 XX  
 XX Streptococcus pyogenes.  
 XX Synthetic.  
 XX  
 XX Key location/Qualifiers  
 XX Peptide 1..30  
 XX /label= sig\_peptide  
 XX 31..250  
 XX /label= mat\_peptide  
 XX  
 XX MO6640930-A1.  
 XX  
 XX 19-DEC-1996.  
 XX  
 XX 07-JUN-1996; 96MO-US10252.  
 XX  
 XX 07-JUN-1995; 95US-0480261.  
 XX  
 XX (MIND ) UNIV MINNESOTA.  
 XX  
 XX Ohlendorf D, Roggliani M, Schlievert PM, Stoeck J;  
 XX WPI: 1997-099936/09.  
 XX  
 XX Mutant SPE-A toxin with at least one amino acid change is  
 XX substantially non-lethal - used in vaccine composition for  
 XX treatment of cancer and streptococcal toxic shock syndrome etc.  
 XX  
 XX Claim 5; Page -: 102pp; English.  
 XX  
 XX The present sequence is a non-lethal Streptococcus pyogenes  
 XX Streptococcal toxin A (SPE-A) mutant, which can be used to produce  
 XX vaccines to protect animals against wild type SPE-A and to treat  
 XX cancer and streptococcal toxic shock syndrome (STSS). The mutant  
 XX SPE-A causes neutralising antibodies (Ab) to be produced, which  
 XX may be used to ameliorate STSS symptoms, e.g. fever, hypotension,  
 XX multiple organ dysfunction, and liver and kidney damage.  
 XX damage. The neutralising Ab is preferably administered in  
 XX conjunction with antibiotic therapy. The mutant SPE-A is  
 XX especially useful for treating T cell lymphomas, and ovarian and  
 XX uterine cancer. It is thought that mutant SPE-A can be selectively  
 XX toxic to T cell lymphoma cells.  
 XX N.B. Sequence not given in the specification, but constructed  
 XX using the wild type SPE-A sequence given on pages 77-79.  
 XX  
 XX Sequence 250 AA:  
 XX  
 XX Query Match 97.5%; Score 1286.5; DB 18; Length 250;  
 XX Best Local Similarity 98.8%; Pred. No. 4.7e-108;  
 XX Matches 248; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 XX  
 XX 1 MNNKKYKLVKMFVYVTEGLTISQVFAQDDPPDSQHRSSLVKMNQITFLYEGCPY 60  
 XX DB 1 MNNKKYKLVKMFVYVTEGLTISQVFAQDDPPDSQHRSSLVKMNQITFLYEGCPY 60  
 XX  
 XX 61 TERNKSVQDLSSHLLIYNVSPYVYKLTKEKNQENAKLTKRKNAVDTGVEYHLCYL 120  
 XX DB 61 TERNKSVQDLSSHLLIYNVSPYVYKLTKEKNQENAKLTKRKNAVDTGVEYHLCYL 120  
 XX  
 XX 121 ENAKRSACITGVYTHNBSNHLIFPKATVYVVISDIOISLDFETNNKAVYAOGLDYVR 180  
 XX DB 121 ENAKRSACITGVYTHNBSNHLIFPKATVYVVISDIOISLDFETNNKAVYAOGLDYVR 180

```

Db      121 EAKERRA-IIGGVNHEGSHLEIPKTIYKVSIDIGISLSPDIETNKKRVTAQELDYKVR 179
      181 KYLDNKOIYTNIGSKETGYIKFIIPNNKESFPPPEPFTQSKYLMITYKDNFTLDSN 240
      180 KYLDNKOIYTNIGSKETGYIKFIIPNNKESFPPPEPFTQSKYLMITYKDNFTLDSN 239
QY      241 TSOIEVYLTKR 251
      240 TSOIEVYLTKR 250
Db
RESULT 15
AAM59798 standard; Protein: 251 AA.
ID      AAM59798;
XX      12-OCT-1998 (first entry)
XX      Amino acid sequence of mutant Streptococcus pyogenes exotoxin A.
DE      SPE-A toxin; nonlethal; mutant: Streptococcus pyogenes exotoxin A;
KM      wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;
KM      streptococcal toxic shock syndrome; STSS; T cell lymphoma;
KM      uterine cancer.
XX      Streptococcus pyogenes.
OS
FH      Key Location/Qualifiers
FT      Misc-difference 20 /note="Optionally Asp, Glu, Tyr, or Arg"
FT      Misc-difference 45 /note="Optionally Asp, Glu, Ser, Thr, or Ala"
FT      Misc-difference 98 /note="Optionally Ser, Ala, Gly, or Thr"
FT      Misc-difference 157 /note="Optionally Glu or Asp"
XX      NO9824911-A2.
XX      11-JUN-1998.
PD      05-DEC-1997: 97NO-US222228.
XX      06-DEC-1996: 96US-0032930.
XX      (MINU) UNIV MINNESOTA.
XX      Ohlendorf D, Roggiani M, Schlievert PW, Stoehr J;
XX      MPI: 1998-33330/29.
XX      New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention
XX      or treatment of streptococcal infection or toxic shock syndrome
PS      Claim 4: Page -: 93pp; English.
XX
CC      This is the amino acid sequence of the mutant Streptococcus pyogenes
CC      exotoxin A (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin
CC      has at least 1 aa change and is nonlethal compared with a protein to
CC      which is referred to as "lethal toxin". The mutant SPE-A toxins are nontoxic and can
CC      produce antitoxin. The mutant SPE-A toxins are nontoxic and can
CC      protect against the development of streptococcal toxic shock syndrome
CC      (STSS). In addition, the toxins can be used for treating animals with
CC      stimulating T cell proliferation and in the treatment of cancer. In
CC      addition, the toxins can be used for treating T cell lymphomas, and ovarian
CC      cancer and uterine cancer.
CC      This sequence was not present in the specification but was created
CC      using information given.

```

```

XX      SQ      Sequence      251 AA:
QY      Query Match      97.4%: Score 1288; DB 19; Length 251;
      Best Local Similarity      97.6%: Fred. No. 5.3e-108;
      Matches      243; Conservative      0; Mismatches      6; Indels      0; Gaps      0;
QY      1 MKNKKVLYKRMVFFVLYTFGLTISQVEPAQOOPDPQSOLNRSIYKNIQNIYFYLEGDPV 60
      1 MKNKKVLYKRMVFFVLYTFGLTISQVEPAQOOPDPQSOLNRSIYKNIQNIYFYLEGDPV 60
Db      61 THENKVSVDLSHLLTNVSGPNTDKLTKANDSNATLPRKANDITGVGYHLCTYC 120
      61 THENKVSVDLSHLLTNVSGPNTDKLTKANDSNATLPRKANDITGVGYHLCTYC 120
QY      121 ENKERSACIYGCVNHEGSHLEIPKTIYKVSIDIGISLSPDIETNKKRVTAQELDYKVR 180
      121 ENKERSACIYGCVNHEGSHLEIPKTIYKVSIDIGISLSPDIETNKKRVTAQELDYKVR 180
Db      181 KYLDNKOIYTNIGSKETGYIKFIIPNNKESFPPPEPFTQSKYLMITYKDNFTLDSN 240
      181 KYLDNKOIYTNIGSKETGYIKFIIPNNKESFPPPEPFTQSKYLMITYKDNFTLDSN 240
QY      241 TSOIEVYLTKR 251
      241 TSOIEVYLTKR 251
Db

```

Search completed: June 23, 2003, 16:12:24  
 Job time : 38.5551 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 16:06:15 : Search time 68.3449 Seconds

(Without alignments) 912.449 Million cell updates/sec

Title: US-10-002-784a-27

Sequence: 2500

Scoring table: 1 MGDPPGSQLHRSLSLVNINQ.....ALGTCGACGCTGCTGSAVVG 468

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 13350620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 43 summaries

Database :	1: A. Genesec-101002:*
1: /SID52/gcgdata/genesec/genesecp-emb1/AA1980.DAT:*	
2: /SID52/gcgdata/genesec/genesecp-emb1/AA1981.DAT:*	
3: /SID52/gcgdata/genesec/genesecp-emb1/AA1982.DAT:*	
4: /SID52/gcgdata/genesec/genesecp-emb1/AA1983.DAT:*	
5: /SID52/gcgdata/genesec/genesecp-emb1/AA1984.DAT:*	
6: /SID52/gcgdata/genesec/genesecp-emb1/AA1985.DAT:*	
7: /SID52/gcgdata/genesec/genesecp-emb1/AA1986.DAT:*	
8: /SID52/gcgdata/genesec/genesecp-emb1/AA1987.DAT:*	
9: /SID52/gcgdata/genesec/genesecp-emb1/AA1988.DAT:*	
10: /SID52/gcgdata/genesec/genesecp-emb1/AA1989.DAT:*	
11: /SID52/gcgdata/genesec/genesecp-emb1/AA1990.DAT:*	
12: /SID52/gcgdata/genesec/genesecp-emb1/AA1991.DAT:*	
13: /SID52/gcgdata/genesec/genesecp-emb1/AA1992.DAT:*	
14: /SID52/gcgdata/genesec/genesecp-emb1/AA1993.DAT:*	
15: /SID52/gcgdata/genesec/genesecp-emb1/AA1994.DAT:*	
16: /SID52/gcgdata/genesec/genesecp-emb1/AA1995.DAT:*	
17: /SID52/gcgdata/genesec/genesecp-emb1/AA1996.DAT:*	
18: /SID52/gcgdata/genesec/genesecp-emb1/AA1997.DAT:*	
19: /SID52/gcgdata/genesec/genesecp-emb1/AA1998.DAT:*	
20: /SID52/gcgdata/genesec/genesecp-emb1/AA1999.DAT:*	
21: /SID52/gcgdata/genesec/genesecp-emb1/AA2000.DAT:*	
22: /SID52/gcgdata/genesec/genesecp-emb1/AA2001.DAT:*	
23: /SID52/gcgdata/genesec/genesecp-emb1/AA2002.DAT:*	

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1327.5	53.1	388	17	AA007898	Streptococcus pyog
2	1327.5	53.1	388	17	AA007898	Streptococcus pyog
3	1327.5	53.1	388	17	AA007898	Streptococcus pyog
4	1323.5	52.0	398	21	AA023572	Streptococcus pyog
5	1195.5	47.8	398	21	AA036098	Streptococcus pyog
6	1136	45.4	251	21	AA070109	Streptococcus pyog
7	1136	45.4	251	22	AA079508	Streptococcus pyog
8	1129	45.2	221	22	AA067344	Streptococcus pyog
9	1123	44.9	221	12	AA013309	Streptococcus pyog
10	1123	44.9	221	14	AA045017	Streptococcus pyog

11	1123	44.9	221	23	AA076240	Streptococcus pyog
12	1122	44.9	251	18	AA012097	Streptococcus pyog
13	1122	44.9	251	19	AA059780	Amino acid sequenc
14	1118	44.9	251	18	AA012154	Streptococcus pyog
15	1118	44.9	251	18	AA012154	Streptococcus pyog
16	1117.5	44.7	250	18	AA012145	Streptococcus pyog
17	1117	44.7	251	18	AA012150	Streptococcus pyog
18	1117	44.7	251	18	AA012146	Streptococcus pyog
19	1113	44.5	251	18	AA012148	Streptococcus pyog
20	1112	44.5	251	18	AA012152	Streptococcus pyog
21	1112	44.5	251	18	AA012153	Streptococcus pyog
22	1112	44.5	251	18	AA012154	Streptococcus pyog
23	1107	44.3	251	19	AA059781	Amino acid sequenc
24	1107	44.3	251	19	AA059788	Amino acid sequenc
25	1107	44.3	251	19	AA059798	Synthetic SSB prot
26	543	21.7	239	19	AA064647	Streptococcus aut
27	541	21.6	239	22	AA067341	Streptococcus aut
28	541	21.6	239	22	AA067341	Streptococcus aut
29	539	21.6	266	21	AA067337	Plant-optimized mu
30	539	21.6	266	21	AA067337	Streptococcus aut
31	530	21.3	266	21	AA070106	Streptococcus aut
32	530	21.2	240	21	AA079505	Streptococcus aut
33	530	21.2	240	21	AA054465	Mutant Streptococ
34	528	21.1	239	12	AA013206	Amino acid sequenc
35	528	21.1	239	14	AA045014	Streptococcus aut
36	527	21.1	239	23	AA076237	Streptococcus aut
37	525	21.0	239	21	AA070106	Mutant Streptococ
38	525	21.0	239	21	AA070106	Streptococcus aut
39	514	20.6	266	21	AA070108	Streptococcus aut
40	514	20.6	266	23	AA079507	Streptococcus aut
41	513.5	20.5	265	21	AA070104	Streptococcus aut
42	513	20.5	239	20	AA065254	Streptococcus aut
43	511	20.4	238	14	AA050136	Streptococcus aut
44	510	20.4	238	13	AA050136	Streptococcus aut
45	510	20.4	238	22	AA076235	Streptococcus aut

## ALIGNMENTS

RESULT 1

ID: AA007898 standard; Protein: 398 AA.

AA007898:

22-JUL-1997 (first entry)

Streptococcus pyogenes clone speb7 pre-pro cysteine protease.

Pre-pro: cysteine; Protease; Inhibition: neoplasia; Proliferation;

Coli: human; tissue: epithelium; carcinoma; melanoma; lymphoma;

leukemia; leukemia; blood; lung; mammary gland; prostate;

Intestine; stomach; liver; heart; skin; pancreas; brain tissue;

wound covering; prevention; metastasis; identification; speb7.

Streptococcus pyogenes.

Key: Location/Qualifiers

Misc-difference 216

FT Domain

W09634941-AL.

07-NOV-1996.

30-APR-1996.

01-MAY-1995.

9505-043692.

(BAYD ) BAYLOR COLLEGE MEDICINE.

PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX Anthrasmawmy HN, Fernandez A, Kapur V, Musser JM;  
 XX WPI. 1996-506148/50.  
 XX N-PSDB; AAT15219.  
 XX  
 PT Use of extracellular streptococcal cysteine protease enzyme - for  
 PT inhibiting the proliferation of neoplastic cells, e.g. for treating  
 PT carcinoma, lymphoma or leukemia.  
 XX  
 XX Disclosure: Pages 59-61; 99pp; English.  
 CC The present sequence is the Streptococcus pyogenes clone spdb7  
 CC pre-pro cysteine protease (CP), which can be used to inhibit  
 CC neoplastic cell proliferation, especially in a human, useful in the  
 CC treatment of neoplastic conditions, e.g. carcinomas, sarcomas,  
 CC melanomas, lymphomas and leukemias originating from blood, lung,  
 CC mammary gland, prostate, intestine, stomach, liver, heart, skin,  
 CC pancreas, bone marrow, and can also be used to prevent metastasis or  
 CC wound covering, and can also be used to prevent metastasis or  
 CC identify susceptible neoplastic cells.  
 CC K1735 and CM519 melanoma cells were injected s.c. into nu/nu mice,  
 CC optionally followed by i.p. injection of CP (100 microm, 24 hours  
 CC later). The mice were checked twice weekly for tumour growth for  
 CC 12 weeks, to give results that showed that treatment with CP  
 CC melanoma growth, and protected 60% of the mice from developing  
 CC CM519 melanomas.  
 XX  
 XX Sequence 398 AA:  
 SQ  
 Query Match 53.1%; Score 1327.5; DB 17; Length 398;  
 Blast Local Similarity 91.3%; Pred. No. 1.5e-99;  
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;  
 OY 192 FTSQXYMLIYKDNFETLSNTOIEVLYLT---KQPVASLLSKGIHYNOGNYMLLTPVI 248  
 DB 120 FMES-YVBOIKENKRLT---TYAGTAEIKQPVVSSLLSKGIHYNOGNYMLLTPVI 173  
 OY 249 EKYVKGDSFVGOHAATGCVAATATQIMKYNTPKMKGLADYTTLSNNFTNPNKALPA 308  
 DB 174 EKYVKGDSFVGOHAATGCVAATATQIMKYNTPKMKGLADYTTLSNNFTNPNKALPA 233  
 OY 309 AISTQYNNMNNILPTYSGRSIVOKVAISELMADVGISTVDMDGPSGSSAGSSVVRALK 368  
 DB 234 AISTQYNNMNNILPTYSGRSIVOKVAISELMADVGISTVDMDGPSGSSAGSSVVRALK 293  
 OY 369 ENGYKNSVHOINSDPS-QDMQEAIDKELSNQNPVYTCG-GYVGAHAPYTDGADSNFTY 426  
 DB 294 ENGYKNSVHOINSDPS-QDMQEAIDKELSNQNPVYTCG-GYVGAHAPYTDGADSNFTY 353  
 OY 427 HVMKMGCVSDGFPRDLALNPSALCTGCGAGCGNGCYOSAVNG 468  
 DB 354 HVMKMGCVSDGFPRDLALNPSALCTGCGAGCGNGCYOSAVNG 395  
 RESULT 2  
 ID AAR95856 standard; Protein: 398 AA.  
 XX AAR95856;  
 XX  
 XX 30-OCT-1996 (first entry)  
 XX  
 XX S. Pyogenes spdb gene encoded extracellular protease.  
 XX  
 XX Immunogenic peptide; spdb gene; extracellular protease; production;  
 XX antibody; vaccine; diagnosis; detection; Streptococcus infection;  
 XX skin infection; acute rheumatic fever; scarlet fever;  
 XX post-streptococcal glomerulonephritis; sepsis; meningitis;  
 XX erysipelas; cellulitis; fasciitis; toxic shock like syndrome.

XX Streptococcus pyogenes.  
 XX Key Location/Qualifiers  
 XX Domain 335..338  
 XX Region 335..338 putative nucleotide binding domain  
 XX Misc-difference 216  
 XX /note= "corresponding codon TAG"  
 XX  
 XX W09608559-A2.  
 XX  
 XX 21-MAR-1996.  
 XX  
 XX 13-SEP-1995; 95W0-US1123.  
 XX  
 XX 14-SEP-1994; 94US-0306542.  
 XX  
 XX (BAYL ) BAYLOR COLLEGE MEDICINE.  
 XX Kapur V, Musser JM;  
 XX WPI. 1996-179944/18.  
 XX N-PSDB; AAT15294.  
 XX  
 XX Use of extracellular protease(s), partic. cysteine protease - for  
 XX detection, diagnosis prevention and treatment of infection by  
 XX pathogenic organisms, partic. gp. A streptococcus strains  
 XX  
 XX Disclosure: Page 12; 97pp; English.  
 XX  
 XX The present sequence is the S. pyogenes spdb gene encoded  
 XX extracellular protease. An immunogenic peptide derived from the  
 XX protease can be used in the prodn. of antibody (Ab) and vaccine. Ab  
 XX can be used to detect the prodn. of the peptide into a human, pred. to mouse.  
 XX followed by Ab isolation. The peptide can be used to prevent  
 XX infections, while vaccine, which inhibits streptococcal  
 XX replication, can be used to prevent and treat gp. A streptococcus  
 XX infections, and partic. to ameliorate pharyngitis, tonsillitis,  
 XX skin infections, acute rheumatic fever, scarlet fever,  
 XX post-streptococcal glomerulonephritis, sepsis, meningitis,  
 XX erysipelas, cellulitis, fasciitis and toxic shock like syndrome.  
 XX  
 XX Sequence 398 AA:  
 SQ  
 Query Match 53.1%; Score 1327.5; DB 17; Length 398;  
 Blast Local Similarity 91.3%; Pred. No. 1.5e-99;  
 Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;  
 OY 192 FTSQXYMLIYKDNFETLSNTOIEVLYLT---KQPVASLLSKGIHYNOGNYMLLTPVI 248  
 DB 120 FMES-YVBOIKENKRLT---TYAGTAEIKQPVVSSLLSKGIHYNOGNYMLLTPVI 173  
 OY 249 EKYVKGDSFVGOHAATGCVAATATQIMKYNTPKMKGLADYTTLSNNFTNPNKALPA 308  
 DB 174 EKYVKGDSFVGOHAATGCVAATATQIMKYNTPKMKGLADYTTLSNNFTNPNKALPA 233  
 OY 309 AISTQYNNMNNILPTYSGRSIVOKVAISELMADVGISTVDMDGPSGSSAGSSVVRALK 368  
 DB 234 AISTQYNNMNNILPTYSGRSIVOKVAISELMADVGISTVDMDGPSGSSAGSSVVRALK 293  
 OY 369 ENGYKNSVHOINSDPS-QDMQEAIDKELSNQNPVYTCG-GYVGAHAPYTDGADSNFTY 426  
 DB 294 ENGYKNSVHOINSDPS-QDMQEAIDKELSNQNPVYTCG-GYVGAHAPYTDGADSNFTY 353  
 OY 427 HVMKMGCVSDGFPRDLALNPSALCTGCGAGCGNGCYOSAVNG 468  
 DB 354 HVMKMGCVSDGFPRDLALNPSALCTGCGAGCGNGCYOSAVNG 395  
 RESULT 3

[illegible]

Db 234 AATSPRYTQNNNNLLPTPGSGESNPQKKALLISELMAALVGIISVMDQSPSSGASSRVOARLK 293

Qy 369 ENFGYINQSGVHQINRSDS-QGMEPAQVDEKLEISQNPVYVQG-GKVGHAIVYIDAGGNNFY 426

Db 294 ENFGYINQSGVHQINRSDS-QGMEPAQVDEKLEISQNPVYVQGSGVGHAAVYIDAGGNNFY 353

Qy 427 HYNNKGWGVSEPPDLALNPSALATGCGAGGFWGQSAVYG 468

Db 354 HYNNKGWGVSEPPDLALNPSALATGCGAGGFWGQSAVYG 395

SEQUENCE 4

ABP29579

ABP29579 standard: Protein: 398 AA.

ABP29579:

02-JUL-2002 (first entry)

Streptococcus polypeptide SEQ ID NO 8334.

Streptococcus GAS: GAS, group A streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibodies; anti-inflammation; infection; vaccine; meningitis; gene therapy.

Streptococcus pyogenes.

W0200234771-A2.

02-MAY-2002.

29-OCT-2001: 2001WO-GB04789.

27-OCT-2000: 2000GB-0026333.

24-NOV-2000: 2000GB-0028727.

07-MAR-2001: 2001GB-0005640.

(CHIR-) CATRON SPA.

(GMO-) INST GENOMIC RES.

Telford J, Maigani V, Margalit Ros YI, Grand G, Fraser C; Telford J;

WI: 2002-352536/38.

N-PSB; ABA70210.

New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -

Claim 1; Page 3948; 4523pp; English.

The invention relates to a protein (ABP5413-ABP20085) from group B streptococcus (GBS (Streptococcus agalactiae)) comprising one of 5483 sequences (S1) given in the specification. The proteins have antibacterial and anti-inflammatory activity. (1), nucleic acid encoding (1), ABA6044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyogenes. Nucleic acid encoding (1) is used to determine whether a compound binds to a biological sample. (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.

Sequence 398 AA:

Query Match 52.9%; Score 1323.5; DB 23; Length 398;  
 Best Local Similarity 91.1%; Pred. No. 3.2e-99;  
 Matches 237; Conservative 5; Mismatches 9; Indels 11; Gaps 5;

192 FTSKRLAIYKDNELLSNTQLEVYLTFT---KQPVVSLDSKGIHYGCFNPLILPTV 248  
 120 FMES YVEQIKENKILDT-----TYGATMEIKQPVVSLDSKGIHYGCFNPLILPTX 173  
 DB 120 FMES YVEQIKENKILDT-----TYGATMEIKQPVVSLDSKGIHYGCFNPLILPTX 173  
 QY 249 EKXKGGDSFVGQHAATGCVAATATQIMKHYNPKGLADYTTLSNNPFYRHPKRLFA 308  
 DB 174 EKXKGGDSFVGQHAATGCVAATATQIMKHYNPKGLADYTTLSNNPFYRHPKRLFA 233  
 QY 309 AISTQYNNNLITPTSGRSNVOKMAISELMADVGISVDMDTGPSSGAGSSRYORALX 368  
 DB 234 AISTQYNNNLITPTSGRSNVOKMAISELMADVGISVDMDTGPSSGAGSSRYORALX 293  
 QY 369 ENGYNOSVHOJNRSDFP-ODMEQAQIDKELLSQNOPVYVYG- GKYGCHAFVYIGADGNRY 426  
 DB 294 ENGYNOSVHOJNRSDFP-ODMEQAQIDKELLSQNOPVYVYG- GKYGCHAFVYIGADGNRY 333  
 QY 427 HYVMKGVSVDGCFRDLALNPSALGTGGAGCFNGTOSAVNG 468  
 DB 354 HYVMKGVSVDGCFRDLALNPSALGTGGAGCFNGTOSAVNG 395

RESULT 5  
 AAB36098 standard: Protein: 398 AA.  
 AAB36098:  
 AAB36098:  
 16-FEB-2001 (first entry)  
 XX  
 DT Streptococcus pyogenes streptolysin.  
 XX  
 DE Streptococcus pyogenes; streptolysin; periodontitis; anti-inflammatory;  
 XX  
 KW antibacterial; amidiolytic; alpha\_1-proteinase inhibitor; periodontitis;  
 XX  
 KM gingivitis.  
 XX  
 OS Streptococcus pyogenes.  
 XX  
 PD WC2000063394-A2.  
 XX  
 PD 26-OCT-2000.  
 XX  
 PF 20-APR-2000: 2000MO-US10574.  
 XX  
 PR 21-APR-1999: 990US-0130436.  
 XX  
 PA (UNICE) UNIV GEORGIA RES FOUND INC.  
 XX  
 PA (TRAV) TRAVIS J.  
 XX  
 PA (POTR) POTEMPA J.  
 XX  
 PA (NELS) NELSON D.  
 XX  
 PI Travis J, Potempa J, Nelson D.  
 XX  
 WP1: 2000-679600/66.  
 XX  
 PT Novel oral bacterial periodontitis polypeptide for treating periodontal  
 PT diseases, has amidolytic activity for cleavage of non-denatured human  
 PT alpha1-proteinase inhibitor at reactive site loop region of inhibitor

Example 1: Fig 1: 55pp; English.

The present sequence is given in a specification relating to novel  
 oral bacterial polypeptide referred to as streptolysin. The polypeptide  
 has amidolytic activity for cleavage of denatured polypeptides and  
 non-denatured serpin polypeptides. It has amidolytic activity for  
 cleavage of a non-denatured human alpha<sub>1</sub>-proteinase inhibitor at a  
 cleavage site loop region of the inhibitor. Proteinase inhibitor is useful for  
 inhibiting the peptidase activity and reducing periodontitis, loss of  
 tooth attachment and periodontal pocket formation, and for reducing

CC growth of bacteria, preferably P. gingivalis in vitro or in vivo.  
 CC It is useful for protecting an animal from a disease caused by  
 CC P. gingivalis and for treating periodontal diseases, including  
 CC gingivitis and periodontitis.  
 XX  
 SO Sequence 398 AA;  
 XX

Query Match 47.8%; Score 1195.5; DB 21; Length 398;  
 Best Local Similarity 84.0%; Pred. No. 8.2e-89;  
 Matches 237; Conservative 5; Mismatches 29; Indels 11; Gaps 5;

192 FTSKRLAIYKDNELLSNTQLEVYLTFT---KQPVVSLDSKGIHYGCFNPLILPTV 248  
 120 FMES YVEQIKENKILDT-----TYGATMEIKQPVVSLDSKGIHYGCFNPLILPTX 173  
 DB 120 FMES YVEQIKENKILDT-----TYGATMEIKQPVVSLDSKGIHYGCFNPLILPTX 173  
 QY 249 EKXKGGDSFVGQHAATGCVAATATQIMKHYNPKGLADYTTLSNNPFYRHPKRLFA 308  
 DB 174 EKXKGGDSFVGQHAATGCVAATATQIMKHYNPKGLADYTTLSNNPFYRHPKRLFA 233  
 QY 309 AISTQYNNNLITPTSGRSNVOKMAISELMADVGISVDMDTGPSSGAGSSRYORALX 368  
 DB 234 AISTQYNNNLITPTSGRSNVOKMAISELMADVGISVDMDTGPSSGAGSSRYORALX 293  
 QY 369 ENGYNOSVHOJNRSDFP-ODMEQAQIDKELLSQNOPVYVYG- GKYGCHAFVYIGADGNRY 426  
 DB 294 ENGYNOSVHOJNRSDFP-ODMEQAQIDKELLSQNOPVYVYG- GKYGCHAFVYIGADGNRY 333  
 QY 427 HYVMKGVSVDGCFRDLALNPSALGTGGAGCFNGTOSAVNG 468  
 DB 354 HYVMKGVSVDGCFRDLALNPSALGTGGAGCFNGTOSAVNG 395

RESULT 6  
 AAY70109 standard: Protein: 251 AA.  
 AAY70109:  
 AAY70109:  
 05-JUN-2000 (first entry)  
 XX  
 DT Streptococcus pyogenic exotoxin A (SPE-A).  
 XX  
 DE Superantigen toxin; SAg; Streptococcus pyogenic exotoxin A; SPE-A;  
 XX  
 KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;  
 XX  
 KM cytotoxic; antibody; streptococcal/streptococcal toxin; toxoid; SPEA4;  
 XX  
 OS Streptococcus sp.  
 XX  
 PD WC2000093154-A1.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 13-AUG-1998: 98MO-US16766.  
 XX  
 PR 13-AUG-1998: 98MO-US16766.  
 XX  
 PA (REED) REED ARMY INST RES WALTER.  
 XX  
 PA (URICH) URICH RG, OLSON MA, BAVARI S.  
 XX  
 PI Ulrich RG, Olson MA, Bavarl S.  
 XX  
 DR N-PSDB: AA251112.  
 XX  
 WP1: 2000-224177/19.  
 XX  
 PT Nucleic acid encoding superantigen toxin useful as a vaccine and for  
 PT diagnosis of superantigen-associated bacterial infections  
 PS

Example 12: Page 94-95; 118pp; English.

The present amino acid sequence is the Streptococcal pyogenic  
 exotoxin A (SPE-A), a bacterial superantigen toxin (Sag), used for the  
 formulation of SPE-A vaccine SP242. The coding region of this Sag toxin  
 is altered by site directed mutagenesis, introducing L24R mutation, that



CC results in disruption of binding of the toxin to both the MHC class II  
 CC or T-cell antigen receptor. SPE-A has antibacterial and cytostatic  
 CC activity. This sequence is useful for the production of SPE-A vaccines  
 CC and specific antibodies. This vaccine overcomes the disadvantages of the  
 CC chemically inactivated toxoids and is designed to protect individuals  
 CC from superantigen-associated bacterial infections.  
 CC It is used for the diagnosis and treatment or amelioration of  
 CC superantigen-associated bacterial infections.

XX Sequence 251 AA/

Query Match 45.4%; Score 1136; DB 21; Length 251;  
 Predicted Similarity 98.2%; Pred. No. 36-84;

Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

DB 2 QDDPSPQJHSSSLVKNLONTITVEGDPPTHEVNSVDQJRSNDLITVNSGPNIDKLKT 61  
 31 QDDPSPQJHSSSLVKNLONTITVEGDPPTHEVNSVDQJRSNDLITVNSGPNIDKLKT 90  
 OY 62 ELKNQEMALTEFKKKNDITGVEYHLCYLENARSACI-GGVTRREGNHLEIPKKIYK 120  
 DB 91 ELKNQEMALTEFKKKNDITGVEYHLCYLENARSACI-GGVTRREGNHLEIPKKIYK 150  
 OY 121 VSITGISTSLSPDLEFNKKAVTMOEDLYVAKRLTDNKKQLYTNGSPKTEGTGTFIPKNKE 180  
 DB 151 VSITGISTSLSPDLEFNKKAVTMOEDLYVAKRLTDNKKQLYTNGSPKTEGTGTFIPKNKE 210  
 OY 181 SFMDFPPEPTGSKYIMIKNDETLDSNT-QIEVYVLTIK 220  
 DB 211 SFMDFPPEPTGSKYIMIKNDETLDSNTQIEVYVLTIK 251

RESULT 7

AB679508 standard; Protein; 251 AA.

XX AB679508:

XX 23-SEP-2002 (first entry)

XX Streptococcal pyrogenic exotoxin A vaccine SPEA2.

XX Exotoxin A; SPEA2; superantigen; antigen; toxin; vaccine;

XX attenuation; mutant; nuclein.

XX Streptococcus pyogenes.

XX Synthetic.

XX US639332-B1.

XX 04-JUN-2002.

XX 01-SEP-1998; 98US-0144776.

XX 25-JUN-1997; 97US-0882431.

XX (USSA ) US SEC OF ARMY.

XX ULRICH RG, OLSON MA, BAWART S;

XX WPI: 2002-546281/58.

XX N-PSDB; ABN84239.

XX Novel isolated and purified superantigen toxin DNA fragment which has  
 XX been genetically altered, useful for producing vaccine for treatment of  
 XX superantigen toxin-associated bacterial diseases

XX Disclosure; Column 63-65; 46pp; English.

XX The present sequence is the protein sequence of Streptococcus  
 CC pyogenes vaccine SPEA2. The vaccine differs from the native SPEA  
 CC sequence by substitution of the Leu-42 residue by Arg. This  
 CC mutation is expected to disrupt contact between the toxin and the

CC HLA-DR receptor, reducing DR1 binding. SPEA2 can be expressed as  
 CC a recombinant protein in *Escherichia coli* as a secreted protein or  
 CC as a cytoplasmic product. No indicators of toxicity have been  
 CC detected for the purified recombinant protein, and vaccine studies  
 CC demonstrate that SPEA2 is highly antigenic, reducing protective  
 CC immunity to superantigen toxin infections.  
 CC be used to protect against superantigen toxin infections. Methods of  
 CC production and using altered superantigen toxins as vaccines, and in  
 CC diagnosis and therapy, are provided by the invention. A multivalent  
 CC vaccine consisting of altered superantigen toxins from SEA, SEB,  
 CC SEC-1, TSEF-1 and SPEA is predicted to provide protective immunity  
 CC against the majority of bacterial superantigen toxins.

XX Sequence 251 AA/

Query Match 45.4%; Score 1136; DB 23; Length 251;  
 Best Local Similarity 98.2%; Pred. No. 36-84;

Matches 217; Conservative 1; Mismatches 1; Indels 2; Gaps 2;

DB 2 QDDPSPQJHSSSLVKNLONTITVEGDPPTHEVNSVDQJRSNDLITVNSGPNIDKLKT 61  
 31 QDDPSPQJHSSSLVKNLONTITVEGDPPTHEVNSVDQJRSNDLITVNSGPNIDKLKT 90  
 OY 62 ELKNQEMALTEFKKKNDITGVEYHLCYLENARSACI-GGVTRREGNHLEIPKKIYK 120  
 DB 91 ELKNQEMALTEFKKKNDITGVEYHLCYLENARSACI-GGVTRREGNHLEIPKKIYK 150  
 OY 121 VSITGISTSLSPDLEFNKKAVTMOEDLYVAKRLTDNKKQLYTNGSPKTEGTGTFIPKNKE 180  
 DB 151 VSITGISTSLSPDLEFNKKAVTMOEDLYVAKRLTDNKKQLYTNGSPKTEGTGTFIPKNKE 210  
 OY 181 SFMDFPPEPTGSKYIMIKNDETLDSNT-QIEVYVLTIK 220  
 DB 211 SFMDFPPEPTGSKYIMIKNDETLDSNTQIEVYVLTIK 251

RESULT 8

AB67344 standard; peptide; 221 AA.

XX AB67344:

XX 23-APR-2001 (first entry)

XX Streptococcus pyogenes toxin A protein.

XX Tumour; cancer; immune; enterotoxin.

XX Streptococcus pyogenes.

XX US610097-B1.

XX 30-JAN-2001.

XX 30-OCT-1998; 98US-0183437.

XX 31-JAN-1994; 94US-0189424.

XX 03-OCT-1985; 89US-0416530.

XX 17-JUN-1990; 90US-0465577.

XX 01-JUN-1991; 91WO-0500342.

XX 02-MAR-1993; 93US-0025144.

XX (TERMA/) TERMAN D S.

XX Terman DS;

XX WPI: 2001-158657/16.

XX Tumor cell capable of stimulating antitumor immune reactivity in vitro  
 XX or in vivo comprises exogenous nucleic acids encoding a superantigen  
 XX and a costimulatory molecule

XX PS Disclosure: Fig 2; 16pp; English.  
 XX CC The present invention relates to a tumour cell capable of stimulating  
 XX CC antitumor immune reactivity. The invention relates to a tumour cell  
 XX CC which expresses an exogenous nucleic acid molecule encoding an antigen  
 XX CC or its active fragment and an exogenous nucleic acid molecule  
 XX CC encoding a costimulatory molecule that activates T cells in  
 XX CC conjunction with an antigenic stimulus. The invention may be used  
 XX CC for cancer therapy by stimulating an anticancer immune response  
 XX CC in vivo or ex vivo.  
 SO Sequence 221 AA;  
 Query Match 45.2%; Score 1129; DB 22; Length 221;  
 Best Local Similarity 97.7%; Pred. No. 9, 2e-84;  
 Matches 215; Conservative 1; Mismatches 2; Indels 2; Gaps 2;  
 QY 2 QOOPPSQLHRSLSLVNKNQNTFFLYRBDPTVHNKSVQQLRSHDLINVSQPNYDKLKT 61  
 DB 1 QOOPPSQLHRSLSLVNKNQNTFFLYRBDPTVHNKSVQQLRSHDLINVSQPNYDKLKT 60  
 QY 62 ELKNDKMTLPFDKNNDIYGVYHLCYLCENAESACI-GGVNREGNHLIPIKRIYVK 120  
 DB 61 ELKNDKMTLPFDKNNDIYGVYHLCYLCENAESACI-GGVNREGNHLIPIKRIYVK 120  
 QY 121 VSDIGISLSPDITKKNVYTAQELDYKVRKYLTDNQLYTNGPSKFTGYIKFIPKNE 180  
 DB 121 VSDIGISLSPDITKKNVYTAQELDYKVRKYLTDNQLYTNGPSKFTGYIKFIPKNE 180  
 QY 181 SFMFDPFPEPPTOSKYLMITYKDNEDTLDSNT-OIEVYLTKK 220  
 DB 181 SFMFDPFPEPPTOSKYLMITYKDNEDTLDSNT-OIEVYLTKK 221  
 RESULT 9  
 AAR13209  
 ID AAR13209 standard; Protein: 221 AA.  
 XX CC AAR13209;  
 XX CC 15-OCR-1991 (first entry)  
 XX CC Streptococcal pyrogenic enterotoxin A.  
 XX CC DE Streptococcal pyrogenic enterotoxin A.  
 XX CC KM SPE A: cancer treatment; pyrogen; tumouricide; scarlet fever.  
 XX CC KM Streptococcus NF-5 strain.  
 XX CC PN MO910680-A.  
 XX CC PD 25-JUL-1991.  
 XX CC PE 17-JAN-1991; 91MO-US00342.  
 XX CC PF 17-JAN-1990; 90US-046577.  
 XX CC PA (TERM/) TERMAN D. S.  
 XX CC PI Terman DS;  
 XX CC WPI: 1991-237984/32.  
 XX CC PT Treating cancer with enterotoxin from *Staphylococcus aureus* -  
 XX CC PT administered by IV injection, having same tumoricidal activity  
 XX CC as *Staphylococcal* protein A without potential toxic reactions  
 XX CC PS Disclosure: Fig 1; 74pp; English.  
 XX CC SPE A can be used for tumoricidal treatment, esp. with a haemolysin.  
 XX CC SYN Synthesis of structural homology to *Streptococcal*  
 XX CC CC pyrogenic exotoxins are claimed  
 XX CC CC statistically significant sequence homology. Alignment of Cysteine

CC residues and similar hydropathy profiles.  
 CC See AAR13203-R13211.  
 XX SO Sequence 221 AA;  
 QY 44.9%; Score 1123; DB 12; Length 221;  
 Best Local Similarity 97.3%; Pred. No. 8e-83;  
 Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;  
 QY 2 QOOPPSQLHRSLSLVNKNQNTFFLYRBDPTVHNKSVQQLRSHDLINVSQPNYDKLKT 61  
 DB 1 QOOPPSQLHRSLSLVNKNQNTFFLYRBDPTVHNKSVQQLRSHDLINVSQPNYDKLKT 60  
 QY 62 ELKNDKMTLPFDKNNDIYGVYHLCYLCENAESACI-GGVNREGNHLIPIKRIYVK 120  
 DB 61 ELKNDKMTLPFDKNNDIYGVYHLCYLCENAESACI-GGVNREGNHLIPIKRIYVK 120  
 QY 121 VSDIGISLSPDITKKNVYTAQELDYKVRKYLTDNQLYTNGPSKFTGYIKFIPKNE 180  
 DB 121 VSDIGISLSPDITKKNVYTAQELDYKVRKYLTDNQLYTNGPSKFTGYIKFIPKNE 180  
 QY 181 SFMFDPFPEPPTOSKYLMITYKDNEDTLDSNT-OIEVYLTKK 220  
 DB 181 SFMFDPFPEPPTOSKYLMITYKDNEDTLDSNT-OIEVYLTKK 221  
 RESULT 10  
 AAR45017  
 ID AAR45017 standard; protein: 221 AA.  
 XX CC AAR45017;  
 XX CC 08-JUN-1994 (first entry)  
 XX CC DT Streptococcal enterotoxin SPE A.  
 XX CC KM SPE A: cancer treatment; pyrogen; tumouricide; scarlet fever.  
 XX CC KM Streptococcal enterotoxin; SE, cancer; tumoricidal agent;  
 XX CC KM autoimmune disease; toxicity; Protein A; perfusion system.  
 XX CC OS *Staphylococcus aureus*.  
 XX CC PN MO9324136-A.  
 XX CC PD 09-DEC-1993.  
 XX CC PE 01-JUN-1993; 93MO-US05213.  
 XX CC PF 01-JUN-1992; 92US-0891718.  
 XX CC PR 01-JUN-1992; 92US-0891718.  
 XX CC PA (STON/) STONE J L.  
 XX CC PA (TERM/) TERMAN D S.  
 XX CC PI Stone JL, Terman DS;  
 XX CC WPI: 1993-405418/50.  
 XX CC DR Use of *Staphylococcal* enterotoxin(s) and homologues - For  
 XX CC DT treatment of cancer in a patient or for the treatment of auto-immune  
 XX CC CC diseases  
 XX CC PS Disclosure: Fig 1; 50pp; English.  
 XX CC The sequences given in AAR45011-21 are *Staphylococcal* enterotoxins (SEs)  
 XX CC CC which may be used in the methods of the invention for treating cancer  
 XX CC CC tumoricidal agents (SEs), and homologues of them, can be used as  
 XX CC CC tumoricidal agents (SEs), and homologues of them, can be used as  
 XX CC CC they exhibit tumoricidal activity and toxicity identical to that  
 XX CC CC observed for the Protein A perfusion system. They may be administered  
 XX CC CC by i.v. injection.  
 XX CC SO Sequence 221 AA;  
 QY 44.9%; Score 1123; DB 14; Length 221;

Best Local Similarity 97.3%; Pred. No. 2.8e-83;  
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;  
OY 2 QODPDPSQLHSSSLVKNLKNITVLESDPYTHENKSVQDLASDHLIVNAGSPNYDKLT 61  
DB 1 QODPDPSQLHSSSLVKNLKNITVLESDPYTHENKSVQDLASDHLIVNAGSPNYDKLT 60  
OY 62 ELKQDMATLFDKNDIDYGEVYHILCYLCENARSACTIGVTRNEGHLETPKPIVX 120  
DB 61 ELKQDMATLFDKNDIDYGEVYHILCYLCENARSACTIGVTRNEGHLETPKPIVX 120  
OY 121 VSIDIGISLSDIETNNKAVTAEOLDYVVKYKLTIDKQOLYTNCPSEKTEGYIFPIKNNK 180  
DB 121 VSIDIGISLSDIETNNKAVTAEOLDYVVKYKLTIDKQOLYTNCPSEKTEGYIFPIKNNK 180  
OY 181 SFMPDLFPEPFPQSKYLMAYKONETLDSNTQIEVYLITRK 220  
DB 181 SFMPDLFPEPFPQSKYLMAYKONETLDSNTQIEVYLITRK 221  
RESUME 11  
AB876240 standard; Protein; 221 AA.  
AC ABB76240;  
XX 09-AUG-2002 (first entry)  
XX 09-AUG-2002 (first entry)  
DE Staphylococcus pyogenes exotoxin A.  
KW Exotoxin A; SPE A; superantigen; antigen; tumour; cancer;  
XX antitumour; therapy.  
XX Streptococcus pyogenes.  
XX US2002051765-A1.  
XX 02-MAY-2002.  
XX 19-DEC-2000; 2000US-0741503.  
XX 31-JUN-1994; 94US-0189424.  
XX 12-JUN-1995; 95US-0189424.  
XX 03-OCT-1989; 89US-0416530.  
XX 17-JUN-1990; 90US-0466577.  
XX 17-JUN-1991; 91MO-US000342.  
XX 01-JUN-1992; 92US-0891718.  
XX 02-MAR-1993; 93US-0025144.  
XX (TERM)/ TERMAN D S.  
XX Terman DS;  
PI WPI: 2002-415198/44.  
DR WPI: 2002-415198/44.  
XX Reagent for treating cancer without the need for e.g. radiotherapy;  
XX comprises a specific V beta subset of T cells sensitized to a growing  
XX tumour and stimulated with superantigens  
XX Disclosure: Fig 2; 17pp; English.  
XX The present sequence is the protein sequence of exotoxin A (SPE A)  
XX of Streptococcus pyogenes. Similarity is shown, in several  
XX instances, between streptococcal enterotoxins, exotoxins  
XX and superantigens, and exotoxins and superantigens. Exotoxins  
XX and superantigens are useful in tumour therapy and in blocking or destroying  
XX autoreactive T and B lymphocyte populations are characterized by  
XX substantial structural homology to streptococcal enterotoxin A and  
XX enterotoxin B, and to streptococcal pyogenic exotoxins, with a  
XX statistically significant sequence homology and similarity (Z value  
XX of Lipman and Pearson algorithm in Monte Carlo analysis exceeding  
XX 6) to include alignment of cysteine residues and similar hydrophobic

profiles. These superantigens are used to treat solid tumours,  
CC including their metastases, without radiation, surgery or  
CC standard chemotherapeutic agents. A claimed method of human cancer  
CC treatment involves contacting hematopoietic cells from a patient  
CC with one or more superantigens that do not generate antitoxic  
CC these cells into the patient to induce an in vivo therapeutic,  
CC tumoricidal reaction.  
XX Sequence 221 AA;  
S0  
Query Match 44.9%; Score 1123; DB 23; Length 221;  
Best Local Similarity 97.3%; Pred. No. 2.8e-83;  
Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;  
OY 2 QODPDPSQLHSSSLVKNLKNITVLESDPYTHENKSVQDLASDHLIVNAGSPNYDKLT 61  
DB 1 QODPDPSQLHSSSLVKNLKNITVLESDPYTHENKSVQDLASDHLIVNAGSPNYDKLT 60  
OY 62 ELKQDMATLFDKNDIDYGEVYHILCYLCENARSACTIGVTRNEGHLETPKPIVX 120  
DB 61 ELKQDMATLFDKNDIDYGEVYHILCYLCENARSACTIGVTRNEGHLETPKPIVX 120  
OY 121 VSIDIGISLSDIETNNKAVTAEOLDYVVKYKLTIDKQOLYTNCPSEKTEGYIFPIKNNK 180  
DB 121 VSIDIGISLSDIETNNKAVTAEOLDYVVKYKLTIDKQOLYTNCPSEKTEGYIFPIKNNK 180  
OY 181 SFMPDLFPEPFPQSKYLMAYKONETLDSNTQIEVYLITRK 220  
DB 181 SFMPDLFPEPFPQSKYLMAYKONETLDSNTQIEVYLITRK 221  
RESUME 12  
AA12097 standard; Protein; 251 AA.  
XX AA12097;  
XX 04-NOV-1997 (first entry)  
XX Streptococcus pyogenes Streptococcal toxin A.  
XX Streptococcal toxin A; SPE-A; non-labile; mutant; production;  
XX vaccine; treatment; cancer; neutralizing antibody;  
XX streptococcal toxic shock syndrome; STSS; symptom; amelloraxitis;  
XX fever; hypotension; group A streptococcal infection; myositis;  
XX fascitis; liver damage; T cell; lymphoma; ovarian; uterine.  
XX Streptococcus pyogenes.  
XX Key Location/Qualifiers  
XX Peptide 1..30  
XX Peptide /label= sig\_peptide  
XX Peptide 31..251  
XX /label= mat\_peptide  
XX W06640930-A1.  
XX 19-DEC-1996.  
XX 07-JUN-1996; 96MO-US10252.  
XX 07-JUN-1995; 95US-0480261.  
XX (MIND ) UNIV MINNESOTA.  
XX Ohlendorf D, Roggliani M, Schlevert PM, Stoehr J;  
XX WPI: 1997-093936/09.  
XX N-PSDB; AA12097.  
XX Mutant SPE-A toxin with at least one amino acid change is  
XX substantially non-lethal - used in vaccine composition for

PT treatment of cancer and streptococcal toxic shock syndrome etc.  
 PS Disclosure: Pages 77-79; 102pp; English.  
 XX  
 CC The present sequence is Streptococcus pyogenes Streptococcal  
 CC toxin A (Spe-A), from which a non-lethal mutant Spe-A, comprising  
 CC at least 1 amino acid change, can be derived. The mutant Spe-A can  
 CC be used to produce vaccines to protect animals against wild type  
 CC Spe-A and to treat cancer and streptococcal toxic shock syndrome  
 CC produced by the mutant Spe-A causes neutralising antibodies (Ab) to be  
 CC produced, which may be used to protect animals against  
 CC fever, hypotension, group A streptococcal infection, myositis,  
 CC fasciitis and liver damage. The neutralising Ab is preferably  
 CC administered in conjunction with antibiotic therapy. The mutant  
 CC Spe-A is especially useful for treating T cell lymphomas, and  
 CC ovarian and uterine cancer. It is thought that mutant Spe-A can be  
 CC selectively toxic to T cell lymphoma cells.  
 XX  
 XX Sequence 251 AA:  
 50  
 Query Match 44.9%; Score 1122; DB 18; Length 251;  
 Best Local Similarity 97.3%; Pred. No. 4, 1e-83;  
 Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;  
 QY 2 QQQPDPQLRRSSLYVKNQNTFYLRBDVYTHENKSVQDLRSHDLINVSQPNYDKLT 61  
 DB 31 QQQPDPQLRRSSLYVKNQNTFYLRBDVYTHENKSVQDLRSHDLINVSQPNYDKLT 90  
 QY 62 ELKNDENALTFPDKNNDIDYGVGYHLCYCENAESACI-GGVYNEEGCNLEIRPKIYVK 120  
 DB 91 ELKNDENALTFPDKNNDIDYGVGYHLCYCENAESACI-GGVYNEEGCNLEIRPKIYVK 150  
 QY 121 VSDIGISLSPDIETKKNVYVQAEIDYKVRKYLTDNQLYTNGPSKYETGYIKETIPKNE 180  
 DB 151 VSDIGISLSPDIETKKNVYVQAEIDYKVRKYLTDNQLYTNGPSKYETGYIKETIPKNE 210  
 QY 181 SFNFDFPPEPPTOSKYLMIYKDNELDLSNT-QIEVYLVTTK 220  
 DB 211 SFNFDFPPEPPTOSKYLMIYKDNELDLSNTQIEVYLVTTK 251  
 RESULT 13  
 AAM59780  
 ID AAM59780 standard; Protein: 251 AA.  
 XX  
 XX AAM59780:  
 AC 12-OCT-1998 (first entry)  
 DT  
 DE Amino acid sequence of Streptococcus pyogenes exotoxin A.  
 XX  
 KM SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;  
 KM wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;  
 KM streptococcal toxic shock syndrome; STSS; T cell lymphoma;  
 KM uterine cancer.  
 XX  
 OS Streptococcus pyogenes.  
 XX  
 PN W09824911-A2.  
 XX  
 PD 11-JUN-1998.  
 XX  
 PF 05-DEC-1997; 97NO-US522228.  
 XX  
 PR 06-DEC-1996; 960US-0032930.  
 XX  
 PA (MINU ) UNIV MINNESOTA.  
 XX  
 XX Ohlendorf D, Roggiani M, Schliavert PM, Stoeck J;  
 XX WPI: 1998-33330/29.  
 DR N-PSDB: AAM41593.  
 XX

PT New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention  
 PS or treatment of streptococcal infection or toxic shock syndrome  
 XX  
 XX Disclosure: Fig 3; 95pp; English.  
 XX  
 CC This is the amino acid sequence of the Streptococcus pyogenes exotoxin A  
 CC (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least  
 CC 1 aa change and is nonlethal compared with a protein to wild type SPE-A  
 CC toxin. The mutant SPE-A toxins are non-toxic and can produce antibodies  
 CC that neutralise wild type SPE-A toxin activity. The toxins can be used  
 CC in vaccines and therapeutics to generate a protective immune response  
 CC against streptococcal infection. They can be used to protect against the  
 CC development of streptococcal infection in conjunction with antibiotics.  
 CC The toxins can be used for treating animals with symptoms of  
 CC streptococcal infection or STSS and in methods for stimulating T cell  
 CC proliferation and in the treatment of cancer. In particular they can be  
 CC used for treating T cell lymphomas, and ovarian and uterine cancer.  
 XX  
 XX Sequence 251 AA:  
 50  
 Query Match 44.9%; Score 1122; DB 19; Length 251;  
 Best Local Similarity 97.3%; Pred. No. 4, 1e-83;  
 Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;  
 QY 2 QQQPDPQLRRSSLYVKNQNTFYLRBDVYTHENKSVQDLRSHDLINVSQPNYDKLT 61  
 DB 31 QQQPDPQLRRSSLYVKNQNTFYLRBDVYTHENKSVQDLRSHDLINVSQPNYDKLT 90  
 QY 62 ELKNDENALTFPDKNNDIDYGVGYHLCYCENAESACI-GGVYNEEGCNLEIRPKIYVK 120  
 DB 91 ELKNDENALTFPDKNNDIDYGVGYHLCYCENAESACI-GGVYNEEGCNLEIRPKIYVK 150  
 QY 121 VSDIGISLSPDIETKKNVYVQAEIDYKVRKYLTDNQLYTNGPSKYETGYIKETIPKNE 180  
 DB 151 VSDIGISLSPDIETKKNVYVQAEIDYKVRKYLTDNQLYTNGPSKYETGYIKETIPKNE 210  
 QY 181 SFNFDFPPEPPTOSKYLMIYKDNELDLSNT-QIEVYLVTTK 220  
 DB 211 SFNFDFPPEPPTOSKYLMIYKDNELDLSNTQIEVYLVTTK 251  
 RESULT 14  
 AAM12154  
 ID AAM12154 standard; Protein: 251 AA.  
 XX  
 XX AAM12154:  
 AC 04-NOV-1997 (first entry)  
 DT  
 DE Streptococcus pyogenes Streptococcal toxin A mutant Ser195A1a.  
 XX  
 KM Streptococcal; toxin A; SPE-A; non-lethal; mutant; production;  
 KM vaccine; protection; treatment; cancer; neutralising antibody;  
 KM streptococcal toxic shock syndrome; STSS; symptom; amelioration;  
 KM fever; hypotension; group A streptococcal infection; myositis;  
 KM fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.  
 XX  
 OS Streptococcus pyogenes.  
 XX  
 PN Synthetic.  
 XX  
 PD Key  
 XX Peptide 1..30 Location/Qualifiers  
 FT 11-251 sig-peptide  
 FT 11-251 mat-peptide  
 FT Misc-difference 225  
 XX /note= "Wild type Ser replaced by Ala"  
 XX  
 XX W09640930-A1.  
 XX  
 PD 19-DEC-1996.  
 XX  
 PR 07-JUN-1996; 96NO-US10252.  
 XX

XX 07-JUN-1995; 950S-0480261.  
 XX (MINI ) UNIV MINNESOTA.  
 XX Ohlendorf D, Roggliant M, Schlievert PM, Stoehr J;  
 XX WPI: 1997-099936/09.  
 XX  
 XX Mutant SPE-A toxin with at least one amino acid change is  
 XX substantially non-lethal - used in vaccine composition for  
 XX treatment of cancer and streptococcal toxic shock syndrome etc.  
 XX  
 XX Example 4: Page -: 102pp; English.  
 XX  
 XX The present sequence is a non-lethal Streptococcus pyogenes  
 XX streptococcal toxin A (SPE-A) mutant, which can be used to produce  
 XX vaccines to protect animals against wild type SPE-A and to treat  
 XX cancer and streptococcal toxic shock syndrome (STSS). The mutant  
 XX SPE-A causes neutralising antibodies (Ab) to be produced, which  
 XX may be used to ameliorate STSS symptoms, e.g. fever, hypotension,  
 XX group A streptococcal infection, myositis, fasciitis and liver  
 XX damage. The neutralising Ab is preferably administered in  
 XX conjunction with antibiotic therapy. The mutant SPE-A is  
 XX especially useful for treating T cell lymphomas, and ovarian and  
 XX uterine cancer. It is thought that mutant SPE-A can be selectively  
 XX N.B. Sequence not given in the specification, but constructed  
 XX using the wild type SPE-A sequence given on pages 77-79.  
 XX  
 XX Sequence 251 AA:  
 XX  
 XX Query Match 44.8% Score 1119; DB 18; Length 251;  
 XX Best Local Similarity 44.8%; Pred. No. 7.2e-93;  
 XX Matches 214; Conservative 2; Mismatches 3; Indels 2; Gaps 2;  
 XX  
 XX 2 QODPDPSQLHRSLSLVKKNQNTYLYEDDPVTHENVASVDLSHDLIYVSGSPNYDKLKT 61  
 XX DB 31 QODPDPSQLHRSLSLVKKNQNTYLYEDDPVTHENVASVDLSHDLIYVSGSPNYDKLKT 90  
 XX QY 62 ELKNOEMATLFDKKNVDIYGVEYHLYCLDENARSACTGGVTHREGNHLIETPKKIYK 120  
 XX DB 91 ELKNOEMATLFDKKNVDIYGVEYHLYCLDENARSACTGGVTHREGNHLIETPKKIYK 150  
 XX QY 121 VASIGIOSLSFDLETNNKWTNOELDRVKAKLIDNDKOLYVNGPKETGYITFPKKNKE 180  
 XX DB 151 VASIGIOSLSFDLETNNKWTNOELDRVKAKLIDNDKOLYVNGPKETGYITFPKKNKE 210  
 XX QY 181 SFMFDFPEPEFQSKLMIYKKNETLDSNTQLEVYLTIK 220  
 XX DB 211 SFMFDFPEPEFQSKLMIYKKNETLDSNTQLEVYLTIK 251  
 XX  
 XX RESULT 15  
 XX AAM12146  
 XX AAM12146 standard; Protein; 251 AA.  
 XX AAM12146:  
 XX 04-NOV-1997 (first entry)  
 XX  
 XX Streptococcus pyogenes Streptococcal toxin A mutant lys157Glu.  
 XX KM streptococcal; toxin A; SPE-A; non-lethal; mutant; production;  
 XX vaccines; protection; treatment; cancer; STSS; myositis;  
 XX streptococcal toxic shock syndrome; STSS; myositis; fasciitis;  
 XX fever; hypotension; group A streptococcal infection; myositis;  
 XX fasciitis; liver damage; T cell; lymphoma; ovarian; uterine.  
 XX KM  
 XX OS Streptococcus pyogenes.  
 XX OS Synthetic.  
 XX Key Location/Qualifiers

FT Peptide 1..30  
 FT Peptide /label- sig\_peptide  
 FT Peptide 31..251  
 FT Misc-difference /label- mat\_peptide  
 FT 187 /note- "wild type lys replaced by glu"  
 XX MO640930-AL.  
 XX  
 XX PD 19-DEC-1996.  
 XX  
 XX PE 07-JUN-1996; 96MO-US010252.  
 XX  
 XX PA 07-JUN-1995; 950S-0480261.  
 XX  
 XX (MINI ) UNIV MINNESOTA.  
 XX Ohlendorf D, Roggliant M, Schlievert PM, Stoehr J;  
 XX WPI: 1997-099936/09.  
 XX  
 XX Mutant SPE-A toxin with at least one amino acid change is  
 XX substantially non-lethal - used in vaccine composition for  
 XX treatment of cancer and streptococcal toxic shock syndrome etc.  
 XX  
 XX Claim 5: Page -: 102pp; English.  
 XX  
 XX The present sequence is a non-lethal Streptococcus pyogenes  
 XX streptococcal toxin A (SPE-A) mutant, which can be used to produce  
 XX vaccines to protect animals against wild type SPE-A and to treat  
 XX cancer and streptococcal toxic shock syndrome (STSS). The mutant  
 XX SPE-A causes neutralising antibodies (Ab) to be produced, which  
 XX may be used to ameliorate STSS symptoms, e.g. fever, hypotension,  
 XX group A streptococcal infection, myositis, fasciitis and liver  
 XX damage. The neutralising Ab is preferably administered in  
 XX conjunction with antibiotic therapy. The mutant SPE-A is  
 XX especially useful for treating T cell lymphomas, and ovarian and  
 XX uterine cancer. It is thought that mutant SPE-A can be selectively  
 XX N.B. Sequence not given in the specification, but constructed  
 XX using the wild type SPE-A sequence given on pages 77-79.  
 XX  
 XX Sequence 251 AA:  
 XX  
 XX Query Match 44.7% Score 1118; DB 18; Length 251;  
 XX Best Local Similarity 46.8%; Pred. No. 8.7e-93;  
 XX Matches 214; Conservative 2; Mismatches 3; Indels 2; Gaps 2;  
 XX  
 XX 1 QODPDPSQLHRSLSLVKKNQNTYLYEDDPVTHENVASVDLSHDLIYVSGSPNYDKLKT 61  
 XX DB 31 QODPDPSQLHRSLSLVKKNQNTYLYEDDPVTHENVASVDLSHDLIYVSGSPNYDKLKT 90  
 XX QY 62 ELKNOEMATLFDKKNVDIYGVEYHLYCLDENARSACTGGVTHREGNHLIETPKKIYK 120  
 XX DB 91 ELKNOEMATLFDKKNVDIYGVEYHLYCLDENARSACTGGVTHREGNHLIETPKKIYK 150  
 XX QY 121 VASIGIOSLSFDLETNNKWTNOELDRVKAKLIDNDKOLYVNGPKETGYITFPKKNKE 180  
 XX DB 151 VASIGIOSLSFDLETNNKWTNOELDRVKAKLIDNDKOLYVNGPKETGYITFPKKNKE 210  
 XX QY 181 SFMFDFPEPEFQSKLMIYKKNETLDSNTQLEVYLTIK 220  
 XX DB 211 SFMFDFPEPEFQSKLMIYKKNETLDSNTQLEVYLTIK 251  
 XX  
 XX Search completed: June 23, 2003, 16:12:25  
 XX Job time : 69.3449 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 16:10:36 : Search time 12.9166 seconds  
(without alignments)

2102.722 Million cell updates/sec

Title: US-10-002-784a-16

Perfect score: 1332  
Sequence: 1 MNKKKKVLAQWFFVLYFL.....KDNFTLDSNTSQIEVITTK 251

Scoring table: Gapop 10.0 / Gapext 0.5

Searched: 417779 segs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\*

1: /cgn2\_5/p/clocata/1/pubpaa/US08.NEM.PUB.PEP.\*  
2: /cgn2\_5/p/clocata/1/pubpaa/US06.NEM.PUB.PEP.\*  
3: /cgn2\_5/p/clocata/1/pubpaa/US06.NEM.PUB.PEP.\*  
4: /cgn2\_5/p/clocata/1/pubpaa/US06.PUBCOMB.PEP.\*  
5: /cgn2\_5/p/clocata/1/pubpaa/US07.NEM.PUB.PEP.\*  
6: /cgn2\_5/p/clocata/1/pubpaa/US07.PUBCOMB.PEP.\*  
7: /cgn2\_5/p/clocata/1/pubpaa/US08.NEM.PUB.PEP.\*  
8: /cgn2\_5/p/clocata/1/pubpaa/US08.PUBCOMB.PEP.\*  
9: /cgn2\_5/p/clocata/1/pubpaa/US09.NEM.PUB.PEP.\*  
10: /cgn2\_5/p/clocata/1/pubpaa/US09.PUBCOMB.PEP.\*  
11: /cgn2\_5/p/clocata/1/pubpaa/US10.NEM.PUB.PEP.\*  
12: /cgn2\_5/p/clocata/1/pubpaa/US10.PUBCOMB.PEP.\*  
13: /cgn2\_5/p/clocata/1/pubpaa/US10.NEM.PUB.PEP.\*  
14: /cgn2\_5/p/clocata/1/pubpaa/US10.PUBCOMB.PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SDMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1322	100.0	251	1	US-08-882-431-16	Sequence 16, App
2	1322	100.0	251	9	US-10-002-784a-16	Sequence 16, App
3	1308	98.9	251	8	US-08-973-391a-13	Sequence 13, App
4	1136	85.9	220	9	US-10-002-784a-26	Sequence 26, App
5	1136	85.9	168	9	US-10-002-784a-27	Sequence 27, App
6	1071	81.4	265	9	US-08-882-431-10	Sequence 10, App
7	576.5	41.6	269	10	US-09-150-478b-12	Sequence 12, App
8	576	43.6	259	10	US-09-150-478b-12	Sequence 12, App
9	575	43.5	266	9	US-10-151-336-8	Sequence 8, App
10	567.5	42.5	266	9	US-10-002-784a-6	Sequence 6, App
11	563	42.6	239	9	US-10-002-784a-10	Sequence 10, App
12	558.5	42.2	266	9	US-10-002-784a-8	Sequence 8, App
13	528	42.2	239	1	US-08-882-431-14	Sequence 14, App
14	528	41.8	266	1	US-10-002-784a-14	Sequence 14, App
15	523	41.8	266	1	US-10-002-784a-14	Sequence 14, App
16	549	41.5	285	1	US-08-882-431-6	Sequence 6, App
17	548	41.5	286	9	US-09-670-759-12	Sequence 12, App
18	542	42.1	285	1	US-08-882-431-8	Sequence 8, App
19	424	32.1	79	9	US-10-002-784a-39	Sequence 39, App

20	340	25.7	258	9	US-09-870-759-14	Sequence 14, App1
21	311	23.5	257	9	US-09-870-759-8	Sequence 8, App1
22	307	23.2	257	1	US-08-882-431-2	Sequence 2, App1
23	307	23.2	257	9	US-10-002-784a-2	Sequence 2, App1
24	291.5	22.0	233	9	US-10-002-784a-4	Sequence 4, App1
25	291.5	22.0	233	9	US-10-002-784a-7	Sequence 7, App1
26	291.5	22.0	233	9	US-10-283-838-7	Sequence 7, App1
27	291.5	22.0	233	9	US-09-900-756-6	Sequence 6, App1
28	289.5	21.9	233	9	US-09-900-756-6	Sequence 6, App1
29	289.5	21.9	233	9	US-10-283-838-8	Sequence 8, App1
30	289	21.9	248	9	US-08-870-759-16	Sequence 16, App1
31	283.5	21.4	233	1	US-08-882-431-4	Sequence 4, App1
32	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
33	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
34	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
35	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
36	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
37	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
38	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
39	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
40	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
41	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
42	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
43	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
44	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1
45	283.5	21.4	233	9	US-08-882-431-4	Sequence 4, App1

## ALIGNMENTS

RESULT 1  
US-08-882-431-16  
Sequence 16, Application US/08882431  
Publication No. US20030009015A1  
GENERAL INFORMATION:  
APPLICANT: MOORE G. WITCHEL,  
APPLICANT: MOORE G. WITCHEL,  
TITLE OF INVENTION: Bacterial Superantigen  
TITLE OF INVENTION: Bacterial Superantigen  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: JOHN MORAN  
CITY: PORT DERRICK  
STATE: MARYLAND  
COUNTRY: USA  
ZIP: 21702-5012  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATOR: APPLE Macintosh  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/882,431  
FILING DATE: June 25, 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Moran, John  
REGISTRATION NUMBER: 26,313  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 619-2065  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 251  
TYPE: Amino Acid  
STRANDEDNESS: Unknown

TOPOLOGY: Unknown  
MOLECULAR TYPE: Peptide  
US-08-892-931-16

Query Match 100.0%; Score 1322; DB 1; Length 251;  
Best Local Similarity 100.0%; Pred. No. 9.5e-110;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MENNKVYLLKMKVFFVLTFLGATLSQDFVACQDPPSQHLHSSLYVKNLQNTYFLYEGSDPV 60  
1 MENNKVYLLKMKVFFVLTFLGATLSQDFVACQDPPSQHLHSSLYVKNLQNTYFLYEGSDPV 60  
DB 61 THENKASVDQLSHDLIYNVSGPYNDKLTETLNDQMATLFPKDNVNDYGVGYTHLCYLC 120  
121 ENHESKACIYGVYTHNECHNLHLEIKRIKVIYKSIDIOSLSFDLETNNKMYTAQGLDYKVR 180  
DB 121 ENHESKACIYGVYTHNECHNLHLEIKRIKVIYKSIDIOSLSFDLETNNKMYTAQGLDYKVR 180  
DB 181 KYTLNKOQLYTNKSGSYETGYIKFIPKNKESFDFPPEPFTQSKYTLMIYKDNQETLSN 240  
DB 181 KYTLNKOQLYTNKSGSYETGYIKFIPKNKESFDFPPEPFTQSKYTLMIYKDNQETLSN 240  
DB 241 TSOIEVYLTK 251  
DB 241 TSOIEVYLTK 251

RESULT 2  
US-10-002-784a-16  
Publication US/10002784A  
Public No. US200303664A1

GENERAL INFORMATION:

33  
APPLICANT: Ulrich, Robert G.  
TITLE OF INVENTION: Bacterial Superantigen Vaccines  
FILE REFERENCE: 003/233/SAP  
CURRENT APPLICATION NUMBER: US/10/002/784A  
CURRENT FILING DATE: 97-06-25; 98-09-01  
PRIOR FILING DATE: 97-06-25; 98-09-01  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: Apple Macintosh Microsoft Word 6.0  
SEQ ID NO 16  
LENGTH: 251  
ORIGIN: Artificial sequence  
FEATURES:  
OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant  
US-10-002-784a-16

Query Match 100.0%; Score 1322; DB 9; Length 251;  
Best Local Similarity 100.0%; Pred. No. 9.5e-110;

Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MENNKVYLLKMKVFFVLTFLGATLSQDFVACQDPPSQHLHSSLYVKNLQNTYFLYEGSDPV 60  
1 MENNKVYLLKMKVFFVLTFLGATLSQDFVACQDPPSQHLHSSLYVKNLQNTYFLYEGSDPV 60  
DB 1 MENNKVYLLKMKVFFVLTFLGATLSQDFVACQDPPSQHLHSSLYVKNLQNTYFLYEGSDPV 60  
DB 61 THENKASVDQLSHDLIYNVSGPYNDKLTETLNDQMATLFPKDNVNDYGVGYTHLCYLC 120  
121 ENHESKACIYGVYTHNECHNLHLEIKRIKVIYKSIDIOSLSFDLETNNKMYTAQGLDYKVR 180  
DB 121 ENHESKACIYGVYTHNECHNLHLEIKRIKVIYKSIDIOSLSFDLETNNKMYTAQGLDYKVR 180  
DB 181 KYTLNKOQLYTNKSGSYETGYIKFIPKNKESFDFPPEPFTQSKYTLMIYKDNQETLSN 240  
DB 181 KYTLNKOQLYTNKSGSYETGYIKFIPKNKESFDFPPEPFTQSKYTLMIYKDNQETLSN 240  
DB 241 TSOIEVYLTK 251

DB 241 TSOIEVYLTK 251

RESULT 3  
US-08-973-391A-13  
Sequence 13, Application US/08973391A  
Patent No. US20020054887A1

GENERAL INFORMATION:

APPLICANT: Schlievert, Patrick M.  
APPLICANT: Stoenig, Jennifer  
APPLICANT: Roggliani, Manuela  
TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE  
FILE REFERENCE: 600.311USNO  
CURRENT APPLICATION NUMBER: US/08/973.391A  
CURRENT FILING DATE: 1998-03-12  
PRIOR FILING DATE: PCT/US96/10252  
PRIOR FILING DATE: 1996-06-07; 96/0480,261  
PRIOR FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 13  
LENGTH: 251  
ORIGIN: Streptococcus pyogenes  
FEATURES:  
OTHER INFORMATION: US-08-973-391A-13

Query Match 98.9%; Score 1308; DB 8; Length 251;  
Best Local Similarity 99.2%; Pred. No. 1.7e-108;

Matches 249; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB 1 MENNKVYLLKMKVFFVLTFLGATLSQDFVACQDPPSQHLHSSLYVKNLQNTYFLYEGSDPV 60  
1 MENNKVYLLKMKVFFVLTFLGATLSQDFVACQDPPSQHLHSSLYVKNLQNTYFLYEGSDPV 60  
DB 61 THENKASVDQLSHDLIYNVSGPYNDKLTETLNDQMATLFPKDNVNDYGVGYTHLCYLC 120  
121 ENHESKACIYGVYTHNECHNLHLEIKRIKVIYKSIDIOSLSFDLETNNKMYTAQGLDYKVR 180  
DB 121 ENHESKACIYGVYTHNECHNLHLEIKRIKVIYKSIDIOSLSFDLETNNKMYTAQGLDYKVR 180  
DB 181 KYTLNKOQLYTNKSGSYETGYIKFIPKNKESFDFPPEPFTQSKYTLMIYKDNQETLSN 240  
DB 181 KYTLNKOQLYTNKSGSYETGYIKFIPKNKESFDFPPEPFTQSKYTLMIYKDNQETLSN 240  
DB 241 TSOIEVYLTK 251  
DB 241 TSOIEVYLTK 251

RESULT 4  
US-10-002-784a-26  
Publication US/10002784A  
Public No. US200303664A1

GENERAL INFORMATION:

33  
APPLICANT: Ulrich, Robert G.  
TITLE OF INVENTION: Bacterial Superantigen Vaccines  
FILE REFERENCE: 003/233/SAP  
CURRENT APPLICATION NUMBER: US/10/002/784A  
CURRENT FILING DATE: 97-06-25; 98-09-01  
PRIOR FILING DATE: 97-06-25; 98-09-01  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: Apple Macintosh Microsoft Word 6.0  
SEQ ID NO 26  
LENGTH: 220  
ORIGIN: Artificial sequence









```

Query Match      42.2% Score 558; DB 1; Length 239;
Best Local Similarity 47.7%; Pred. No. 6,7e-42;
Matches 113; Conservative 39; Mismatches 69; Indels 16; Gaps 5;

QY 30 AODPDSQIHRSS-LYKNAQITFLIEDPQTHENKESYQULASIDITVYNSGP---NY 85
DB 2 SODPDRDELHKSSTCKCKEMKNKLYLDONHVEASLNTKSIDQFMYDLTISIKOTKIGY 61
QY 86 DKLTELKNOEMATLEFKKNVNDIYGVETYLHCYLENA-----ERSACITGVYTH 136
DB 63 DNAREFRKNMDLAKTKOKYVDSGASNAALVTCQESKATYNDINSQTDKRTKCTGAYTH 121
QY 137 ESMHLEIPKKYIVVSIQCIQSLSPIETENKKNVYAOELDYVYKXLYLTDKMOYLTGNSPK 196
DB 122 NGMDQIKRSITVVEFDGKNLLSPDYOTNKKVYAOELDYTRHYLVKDKKLTFFNNSP 181
QY 197 YETGYIKFKPKKESFMEFDFPEP--EFTOSKTYLKYONETLDSNTSQTSEVLYTRK 251
DB 182 YETGYIKFKPKKESFMEFDFPEP--EFTOSKTYLKYONETLDSNTSQTSEVLYTRK 237

RESULT 14
US-08-882-431-14
Sequence 14, Application US/08882431
Publication No. US2003005015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Baverl
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
ADDRESS: 504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM: disk
OPERATING SYSTEM: Apple Macintosh
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
PRIORITY DATA:
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
STRAND: Sense
STRANDNESS: Acid
STRANDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-14

```

```

DB 12 LIFALIVLETPNVLAE---SODPDRDELHKSSTCKCKEMKNKLYLDONHVEASLNTKSIDQFMYDLTISIKOTKIGY 61
QY 69 DOLARSHDIYVNSG--PNYDKLTELKNOEMATLEFKKNVNDIYGVETYLHCYLEC--ENA 123
DB 69 DKRPAHDILYNSKLANDKKTELLEKGLKADYVDYGSNTVYKNCYSSKQV 128
QY 124 ER---SACITGVYTHENKESYQULASIDITVYNSGP---NY 85
DB 129 GKVTGKTCMYGTGITHESGHNPDONLQVILYVEKKNRNTISFEVQDKKSVYAOELDI 168
QY 178 KRYKYLTDNKKOLYTNQPSKESFYETGYIKFKPKKESFMEFDFPEP--EFTOSKTYLKYONET 235
DB 179 KANLEILKNNLYLFEFSSFEYETGYIKFKPKKESFMEFDFPEP--EFTOSKTYLKYONET 248
QY 236 TLDSTNSQIYVLYTRK 251
DB 249 TVDSKSVKIVLYTRK 264

RESULT 15
US-10-002-784a-14
Sequence 14, Application US/10002784A
Publication No. US2003003664A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Baverl
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIORITY DATA: 97-06-25; 98-09-01
FILING DATE: June 25, 1997
PRIORITY DATA:
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
STRAND: Sense
STRANDNESS: Acid
STRANDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-10-002-784a-14

```

```

Query Match      41.8% Score 553; DB 9; Length 266;
Best Local Similarity 44.9%; Pred. No. 2,2e-41;
Matches 115; Conservative 51; Mismatches 72; Indels 18; Gaps 8;

QY 11 WVF-FYLVFPLGLISQEVPAQDDPDSQLHRSYLVNKL-QNITFLYEGDPYTHENKSV 68
DB 12 LIFALIVLETPNVLAE---SODPDRDELHKSSTCKCKEMKNKLYLDONHVEASLNTKSIDQFMYDLTISIKOTKIGY 61
QY 69 DOLARSHDIYVNSG--PNYDKLTELKNOEMATLEFKKNVNDIYGVETYLHCYLEC--ENA 123
DB 69 DKRPAHDILYNSKLANDKKTELLEKGLKADYVDYGSNTVYKNCYSSKQV 128
QY 124 ER---SACITGVYTHENKESYQULASIDITVYNSGP---NY 85
DB 129 GKVTGKTCMYGTGITHESGHNPDONLQVILYVEKKNRNTISFEVQDKKSVYAOELDI 168
QY 178 KRYKYLTDNKKOLYTNQPSKESFYETGYIKFKPKKESFMEFDFPEP--EFTOSKTYLKYONET 235
DB 179 KANLEILKNNLYLFEFSSFEYETGYIKFKPKKESFMEFDFPEP--EFTOSKTYLKYONET 248
QY 236 TLDSTNSQIYVLYTRK 251
DB 249 TVDSKSVKIVLYTRK 264

Search completed: June 23, 2003, 16:16:38
Job time : 13.916 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 16:10:06 : Search time 18.5021 seconds

(without alignments)  
1304.163 Million cell updates/sec

Title: US-10-002-784a-16

Perfect score: 1322  
Sequence: 1 MENNKVKKKWPFVLTFL.....KDNETLDNSTSOLEVLTTR 251

Scoring table: BL0SDM62  
Gapop 10.0, Gapext 0.5

Searched: 263224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 263224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Minimum Match 1008  
Listing first 45 summaries

Database :

1: PIR.\*  
2: PIR.\*  
3: PIR.\*  
4: PIR.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1315	99.5	251	1	exotoxin type A pr
2	1239	93.7	236	2	exotoxin type A pr
3	1234	93.3	236	2	exotoxin type A pr
4	1109	83.9	236	2	exotoxin A precurs
5	1076	81.4	250	1	streptococcal pyro
6	576.5	41.5	266	2	enterotoxin B prec
7	551.5	41.7	266	2	enterotoxin C-2 pr
8	548	41.5	266	2	enterotoxin C-1 pr
9	548	41.5	266	2	enterotoxin C-1 pr
10	440	36.4	258	2	enterotoxin D prec
11	340	25.7	258	2	enterotoxin D prec
12	335	25.5	190	2	enterotoxin F2A2
13	335	25.5	190	2	enterotoxin F2A2
14	336	25.4	260	2	enterotoxin S6A1
15	311.5	23.6	258	2	enterotoxin A prec
16	308	23.3	257	2	enterotoxin A prec
17	307	23.2	257	2	enterotoxin A prec
18	305.5	23.1	240	2	enterotoxin S6A1
19	264	20.0	239	2	enterotoxin S6A1
20	264	20.0	239	2	enterotoxin S6A1
21	211	16.0	233	2	enterotoxin S6A1
22	174	13.2	133	2	enterotoxin S6A1
23	129.5	9.8	231	2	hypothetical prote
24	128	9.7	157	2	hypothetical prote
25	125	9.5	227	2	hypothetical prote
26	114	8.6	232	2	exotoxin 13 [impor
27	114	8.6	234	2	exotoxin 10 [impor
28	114	8.6	234	2	exotoxin 9 [impor
29	111	8.4	292	2	exotoxin 9 [impor

## ALIGNMENTS

RESULT 1

529659

exotoxin type A precursor (allele 1) - Streptococcus pyogenes phase T12

N:Alternate names: erythrogenic toxin; scarlet fever toxin

C:Species: Streptococcus pyogenes phase T12

C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text-change 10-Sep-1999

R:Weeks: 529659 #S18782; S18784; S18785; S18791; S18796; S18800

R:Weeks: C.R. Perrett 1996

Infect. Immun. 52, 144-150, 1986

A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin

A:Reference number: 529659; MUID:8616804; PMID:3314452

A:Accession: S29659

A:Molecule type: DNA

A:Residues: 11251 <MEM>

A:Residues: 11251 <MEM>

R:Wilson, R.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.

J. Exp. Med. 174, 1271-1274, 1991

A:Title: Characterization and clonal distribution of four alleles of the speA gene en

A:Reference number: S18782; MUID:9204323; PMID:1940804

A:Accession: S18782

A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 924 <MEM>

A:Molecule type: DNA

A:Residues: 924 <MEM>

A:Cross-references: EMBL:J61556; NID:947291; PIDN:CAA43754.1; PID:947292

A:Experimental source: Streptococcus pyogenes strain KGS156 isolate Nebraska unassig

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18785

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 924 <MEM>

A:Cross-references: EMBL:J61555; NID:947293; PIDN:CAA43753.1; PID:947294

A:Experimental source: Streptococcus pyogenes strain KGS157 isolate Texas unassigned

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18791

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 924 <MEM>

A:Cross-references: EMBL:J61555; NID:947290; PIDN:CAA43753.1; PID:947310

A:Experimental source: Streptococcus pyogenes strain KGS157 isolate Arizona unassign

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199

A:Accession: S18796

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 924 <MEM>

A:Cross-references: EMBL:J61557; NID:947319; PIDN:CAA43755.1; PID:947320





OY 181 KYTLNNKOLYTNNGSKYETGYIKRPIPRKNKSEFWDFPEPEPQSTQKLYIMYDNEITLSDN 240  
 DB 180 KYTLNNKOLYTNNGSKYETGYIKRPIPRKNKSEFWDFPEPEPQSTQKLYIMYDNEITLSDN 239  
 OY 241 TSDIEVLTTR 251  
 DB 240 TSDIEVLTTR 250  
 RESULT 6  
 ENSA6  
 enterotoxin B precursor - Staphylococcus aureus  
 C:Species: Staphylococcus aureus  
 C>Date: 24-Apr-1984 #sequence\_revision 15-Oct-1996 #text\_Change 16-Jun-1999  
 C:Accession: S27260; A92065; S27240; A01815  
 J. Bacteriol. 166, 29-33, 1986  
 A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.  
 A:Reference number: S27360; M01D:86168023; PMID:3957869  
 A:Accession: S27260  
 A:Residues: 1-266 <CHO>  
 A:Status: preliminary  
 A:Cross-references: EMBL:M1118; NID:9152999; P1DN:AAA8550.1; PID:9153000  
 A:Experimental source: strain 56  
 R.Huang, I.Y.; Bergdoll, M.S.  
 J. Biol. Chem. 245, 3518-3525, 1970  
 A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide  
 A:Accession: A92065  
 A:Residues: A92065; M01D:1007902; PMID:5470821  
 A:Molecule type: protein  
 A:Residues: 28-55; NMD:59-68; 'NE', '71', 'FDLTYL', '78-117', '119-127', 'W', '129', 'D', '131-132', 'ENW',  
 A:Experimental source: strain S-6  
 R.Huang, I.Y.; Bergdoll, M.S.  
 J. Biol. Chem. 245, 3511-3517, 1970  
 A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition,  
 A:Reference number: A92063; M01D:71007900; PMID:5470819  
 J. Biol. Chem. 245, 3493-3510, 1970  
 R.Huang, I.Y.; Bergdoll, M.S.  
 A:Contents: annotation; tryptic peptides  
 A:Reference number: A92063; M01D:71007900; PMID:5470819  
 A:Title: Purification of staphylococcal enterotoxin B.  
 A:Reference number: A90548; M01D:66033792; PMID:4953312  
 A:Contents: annotation; biological source of protein  
 R.Alekshov, V.Y.; Klishay, E.Y.; Kolosov, M.I.; Meuser-Fogel, I.; Moskaleva, E.Y.; Sveshnik  
 Eur. J. Biochem. 209, 823-828, 1992  
 A:Reference number: S27240; M01D:9304338; PMID:1435690  
 A:Accession: S27240  
 A:Molecule type: protein  
 A:Residues: 28-42; 128-148 <NLA>  
 C:Superfamily: enterotoxin B  
 C:KeyWords: enterotoxin; extracellular protein; toxin  
 F:28-266; domain: signal sequence; status predicted <S>  
 F:120-266; domain: signal sequence; status predicted <S>  
 F:120-140; domain: signal sequence; status predicted <S>  
 F:120-140; domain: signal sequence; status predicted <S>  
 Query Match 43.6%; Score 576.5; DB 1; Length 266;  
 Best Local Similarity 48.7%; Pred. No. 1.1e-35;  
 Matches 123; Conservative 38; Mismatches 75; Indels 19; Gaps 7;  
 OY 15 VLVETLGLTIS-OEFA--QDDPPQSLHRS-LVKN--ONTLYEGDPYTHENYSVDQ 70  
 DB 11 ILIFALVILVSPVLAESOPRPLHLSKFGGLGKMKVLYVDNHNSAIVASIDQ 70  
 OY 71 LRSHDLIYVNSG---NTDKLTEKLNKPATLFDKNDVYGVGYHLGYICSA----123  
 DB 71 FLVHDLIYVNSDKKLNDKVTETLDELAKKMDVYDVSNTYVYSSKDNCK 130  
 OY 124 -----EKSACIYGVATNHSNHLIRKTIYKVSIDQISLSPDIEFNKANTVAGLEDTK 178

DB 131 SHOTKRTKTCYGGVETENNOIDKRSYITVYFVDDCKLSTSDVOTKREKTYAGLEDTL 190  
 OY 179 VRKYLTDNNKOLYTNNGSKYETGYIKRPIPRKNKSEFWDFPEPE--EFTQSKLYIMYDNEIT 236  
 DB 191 TRHLLKNNKLLTFERNKSPFETGYIKRPIPRKNKSEFWDFPEPE--EFTQSKLYIMYDNEIT 249  
 OY 237 LDSNTSOIEVLTTR 251  
 DB 250 VDSKDKVKEVLTTR 264  
 RESULT 7  
 S1185  
 enterotoxin C3 - Staphylococcus aureus  
 C:Species: Staphylococcus aureus  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_Change 16-Jul-1999  
 C:Accession: S1185  
 R.Hovde, C.J.; Hackett, S.P.; Bohach, G.A.  
 Mol. Gen. Genet. 220, 329-333, 1990  
 A:Title: Nucleotide sequence of the enterotoxin C3 gene: sequence comp  
 A:Reference number: S1185; M01D:9020508; PMID:2325627  
 A:Accession: S1185  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-266 <CHO>  
 A:Cross-references: GB:X5161; NID:946570; P1DN:CAA3972.1; PID:946571  
 C:Superfamily: enterotoxin B  
 Query Match 41.7%; Score 551.5; DB 2; Length 266;  
 Best Local Similarity 46.1%; Pred. No. 7.7e-34;  
 Matches 117; Conservative 46; Mismatches 74; Indels 17; Gaps 8;  
 OY 15 VLVETLGLTIS-OEFAQDDP--PSQLHRS-LVKNONTLYEGDPYTHENYSVDQ 70  
 DB 11 ILIFALVILVSPVLAESOPRPLHLSKFGGLGKMKVLYVDNHNSAIVASIDQ 70  
 OY 71 LRSHDLIYVNSG---NTDKLTEKLNKPATLFDKNDVYGVGYHLGYIC--ENMR 125  
 DB 71 FLVHDLIYVNSDKKLNDKVTETLDELAKKMDVYDVSNTYVYSSKDNCK 130  
 OY 126 ---SACIYGVATNHSNHLIRKTIYKVSIDQISLSPDIEFNKANTVAGLEDTK 179  
 DB 131 VDSKDKVKEVLTTR 251  
 OY 180 RYLDNDKOLYTNNGSKYETGYIKRPIPRKNKSEFWDFPEPE--EFTQSKLYIMYDNEIT 237  
 DB 191 RNLFLKNNKLLTFERNKSPFETGYIKRPIPRKNKSEFWDFPEPE--EFTQSKLYIMYDNEIT 249  
 OY 238 DSNSTSOIEVLTTR 251  
 DB 251 DSKSKIEVLTTR 264  
 RESULT 8  
 A60114  
 enterotoxin C-2 precursor - Staphylococcus aureus  
 C:Species: Staphylococcus aureus  
 C>Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_Change 16-Jul-1999  
 C:Accession: A60114; B60114; A3866  
 R.Bohach, G.A.; Schlievert, P.M.  
 Infect. Immun. 57, 2249-2257, 1989  
 A:Title: Conservation of the biologically active portions of staphylococcal enterotox  
 A:Reference number: A60114; M01D:8927549; PMID:2536367  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-266 <BOH>  
 A:Accession: B60114  
 A:Molecule type: protein  
 A:Residues: 28-66 <BOH>  
 R.Couch, J.L.; Boley, M.J.





[illegible]

C>Date: 10-May-2001 #sequence\_revision 10-May-2003 #text\_change 22-Oct-2001  
C/Accession: AB996501  
R/Kuroda, M.: Ohta, T., Uchiyama, I.: Babo, T.: Yuzawa, H.: Kobayashi, I.: Cui, E.  
K. Akiuchi, M.: Matsuda-Uoi, Y.: Kobayashi, N.: Sawano, T.: Inoue, R.: Kato, C.: Sa-  
lonche, J.S.T.: 12/5/2001/2001.: Ogasawara, N.: Hayashi, H.: Hirata-Tsu, K.  
A>Title: Whole genome sequencing of melicillin-resistant *Staphylococcus aureus*.  
A/Reference number: AB9758; NUID:23131992; PMID:1145146  
A/Accession : AB9965  
A>Status: preliminary  
A/Molecule type: DNA  
A/Sequence type: full length  
A/Cross-references: NCBI:AB990018; PDB:1J3O;619; PTDN:BABA2912.1; SSPB:GM00149  
A/Experimental source: strain NJ15  
C/Gene(s):  
A/Gene: yentZ

```

0y 125 RAAQITQVGNHSHL-----ELPKYUYUYIDGLOSIEDITNKAWYTAQOELDK 178
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    2 KATQMGAGVEHDGQIDANNSTDHSHILIKYENENHNSPDITPKKNNITAOELDK 61
    3 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0y 179 VNYLIDKCOLQYVNGPKATGQYIKFTFKPKNSFVFQPE--PEFTOSQYVLYADNET 246
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
    2 62 VANYLAKKMLIENRSPPEGLTIFTEGSHSFWTDLAPBSGKRPYVLYLLYMDKT 121
    3 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0y 237 LDSVTSQLELYVLYLTK 251
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0b 122 VESKASINVEVHLTK 136
    1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

R:Kurdo, M., Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, B.; Koyanashi, I.; Cui, M. A.; Mizukami, D. Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekine, H.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuyu, K. C. Genome analysis of *Staphylococcus aureus* strain 359-1, 125-1 and 125-2.  
 L:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
 A:Reference number: AB9758; PMID:21311992; PMID14181460  
 A:Accession: C89584  
 A>Status: preliminary  
 A:Feature type: DNA  
 A:Read length: 350  
 A:Cross-references: DB:BN00018; PID:913701743; PIDN:BNAB3036.1; GSPDB:GNO0149  
 A:Experimental source: strain N315  
 C:Genetics:  
 A:Gene: sep  
 C:Superfamily: enterotoxin B  
 Query Match 25.4% Score 336 DB 2 Length 260  
 Best Local Similarity 34.1% 73-se-18  
 Matches 91 Conservative 55 Mismatch 28  
 Mismatch 28



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 16:06:40 ; Search time 9,77469 Seconds

(without alignments) 1065.033 Million cell updates/sec

Title: US-10-002-784a-16

Sequence: 1 MKNKKVKKMKWFFVLTWL.....KQNETJDSNTSGIEXVLTWK 231

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 segs, 41476320 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40\*

Pred. No. 15 the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1315	99.5	251	1	SPEA_STRPY
2	376.5	43.6	266	1	ETXA_STAU
3	549	41.5	266	1	ETXC_STAU
4	549	41.5	266	1	ETXC_STAU
5	481	36.4	258	1	ETXC_STAU
6	481	36.4	258	1	ETXC_STAU
7	340	25.7	258	1	ETXC_STAU
8	308	23.3	257	1	ETXA_STAU
9	307	23.3	257	1	ETXA_STAU
10	213	16.3	235	1	SPEC_STRPY
11	213	16.3	235	1	SPEC_STRPY
12	165	12.5	234	1	SPEC_STRPY
13	109	8.2	234	1	TSTRT_STAU
14	105.5	7.9	190	1	USOI_YEAST
15	105.5	7.9	894	1	USOI_HUMAN
16	103.5	7.8	396	1	PRRC_ECOLI
17	98	7.4	908	1	DPOL_BOVIN
18	98	7.4	807	1	W2A_SSVIV
19	94.5	7.1	2151	1	RRPL_SEOIN
20	94.5	7.1	2151	1	RRPL_SEOIN
21	93.5	7.1	509	1	HQZ2_HAELN
22	93	7.0	405	1	TACZ_CLOPE
23	92.5	6.9	405	1	DBR1_YEAST
24	91	6.9	303	1	VANT_YEAST
25	90.5	6.8	1593	1	DSCL_BOVIN
26	90.5	6.8	1593	1	DSCL_BOVIN
27	89.5	6.8	722	1	PRSA_MOUSE
28	89.5	6.8	2410	1	POL2_CLOPE
29	89	6.7	554	1	Y7L8_RICPR
30	88.5	6.7	357	1	SPIL_RAPU
31	88.5	6.7	495	1	V243_AQAEV
32	88.5	6.7	540	1	MTAL_AGCA
33	88.5	6.7	993	1	HQBC_HAELN

## ALIGNMENTS

RESULT 1	SPEA_STRPY	STANDARD:	PRT:	251 AA.
ID	SPEA_STRPY			
DT	01-MAR-1988 (Rel. 08, Created)			
DT	01-JUN-1990 (Rel. 13, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)			
DE	(SPE A).			
GN	SPEA OR SPY18_0393.			
OS	Streptococcus pyogenes, and			
OS	Streptococcus pyogenes (serotype M18).			
OC	Bacteri: Firmicutes; Lactobacillales; Streptococcaceae;			
OC	Streptococcus.			
NCBI_Textid-1314, 186103:				
LN	[1]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE-8616804; PubMed-3514452;			
RA	Weaks C.R., Retseck J.J.			
RA	et al. (1986) The type A streptococcal exotoxin			
RT	(erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage			
RT	112.*			
LN	[2]			
RP	Infect. Immun. 52:144-150(1986).			
LN	[3]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE-86284313; PubMed-3526093;			
RA	Johnson C.C., Litalien J.J., Schlivert P.M.			
RA	et al. (1986) The type A streptococcal exotoxin is			
RT	related to streptococcus aureus enterotoxin B.*			
LN	[4]			
RP	Mol. Gen. genet. 203:354-356(1986).			
LN	[5]			
RP	SEQUENCE FROM N.A.			
RP	MEDLINE-86284313; PubMed-3526093;			
RA	Johnson C.C., Litalien J.J., Schlivert P.M.			
RA	et al. (1986) The type A streptococcal exotoxin is			
RT	related to streptococcus aureus enterotoxin B.*			
LN	[6]			
RP	group A Streptococcus strains associated with acute rheumatic fever			
RT	outbreaks.*			
LN	[7]			
RP	Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).			
LN	[8]			
RP	X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).			
RP	MEDLINE-99094887; PubMed-9878045.			
RA	Papageorgiou A.C., Collins C.M., Gorman D.M., Kline J.B.,			
RA	O'Brien S.M., Trenter H.S., Acharya K.R.			
RT	et al. (1999) Structural basis for the recognition of superantigen streptococcal			
RT	pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell			
LN	DB03.116.9-21(1999).			
LN	[9]			
RP	-1- SUBUNIT: Binds to major histocompatibility complex class II beta			
LN	chain.			
CC	-1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE			
CC	THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET			
CC	FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE			

34	88.5	6.7	2412	1	POL1_BAYNG	004574 barley yell
35	88	6.7	181	1	RM06_AGACA	P46765 acanthamoeb
36	87.8	6.7	970	1	I277_WYGE	Q49409 mycoplasma
37	87.5	6.6	449	1	TIG_OJERA	Q39364 ureaplasma
38	87.5	6.6	449	1	RSD1_YEAST	Q04234 saccharomyc
39	87.5	6.6	138	1	RSD1_YEAST	Q04234 saccharomyc
40	87	6.6	715	1	VGL_SSVIV	P15692 apicomplasma
41	87	6.6	1109	1	POL2_CLOPE	P31693 caprine art
42	86.5	6.5	502	1	Y752_BOBIN	Q51693 bovine art
43	86.5	6.5	735	1	YND7_SCIPH	Q10432 schistosom
44	86.5	6.5	1336	1	YH37_YEAST	P48561 saccharomyc
45	86	6.5	407	1	NQDM_OROME	P41928 drosophila

DT 15-JUN-2002 (Ref. 41, Last annotation update)  
DE Enterotoxin type B precursor (SEB).  
GN SEB.  
OS Staphylococcus aureus.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
RX MEDLINE-86168029; PubMed-3957869;  
RN [1]  
RT SEQUENCE FROM N.A.  
RT MEDLINE-86168029; PubMed-3957869;  
RX Jones C.L., Khan S.A.;  
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus  
RT aureus";  
RN [2]  
RT Bacteriol. 166:29-33(1986).  
RX MEDLINE-40-91 FROM N.A.  
RX MEDLINE-85398255; PubMed-3898073;  
RT Rannell D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;  
RT "Molecular cloning of staphylococcal enterotoxin B gene in  
RT Escherichia coli and Staphylococcus aureus";  
RN [3]  
RT Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).  
RX MEDLINE-28-266 (S-6).  
RX MEDLINE-71007902; PubMed-5470821;  
RT Huang I.-Y., Bergdoll M.S.;  
RT "The primary structure of staphylococcal enterotoxin B. 3. The  
RT cytochrome bromide peptides of reduced and aminoethylated enterotoxin  
RT B, and the complete amino acid sequence";  
RN [4]  
RT J. Biol. Chem. 245:3518-3525(1970).  
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RX MEDLINE-93069291; PubMed-1436058;  
RT Swaminathan S., Fucy W.F. Jr., Fletcher J., Sax M.;  
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen";  
RN [5]  
RT Nature 359:801-806(1992).  
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.  
RX MEDLINE-940328; PubMed-815513;  
RT Janderzky T.S., Brown J.B., Grcia J.C., Stern L.J., Urban R.G.,  
RT Chl Y.I., Staefelacher C., Strominger J.L., Wiley D.C.;  
RT "Three-dimensional structure of a human class II histocompatibility  
RT molecule complexed with superantigen";  
RN [6]  
RT Nature 368:711-718(1994).  
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.  
RX MEDLINE-9306289; PubMed-819137;  
RT Li H., Liere A., Rausch P., Leder L., Yeern X., Schleier P.M.,  
RT Karijalainen K., Matzura R.A.;  
RT "Three-dimensional structure of the complex between a T cell receptor  
RT beta chain and the superantigen staphylococcal enterotoxin B";  
RN [7]  
RT Immunity 9:807-816(1998).  
RX X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).  
RX MEDLINE-818101; PubMed-55133;  
RT Pappasogian A.C., Trenter H.S., Acharya K.R.;  
RT "Crystal structure of the microbial superantigen staphylococcal  
RT enterotoxin B at 1.5-A resolution: implications for superantigen  
RT recognition by MHC class II molecules and T-cell receptors";  
RN [8]  
RT J. Mol. Biol. 277:61-79(1998).  
RX -1- SUPERCLASS LOCATION: Secreted.  
RX -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
RX -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN  
RX FAMILY.  
CC THIS SMIS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed, usage by and for commercial  
CC or send an email to license@ebi.ac.uk.  
CC EMBL: M11118; AAA88550.1; -

DR	PIR:	A01815:	ENSBAB.
DR	PIR:	S27360:	S27360.
DR	PDB:	1SEB:	20-JUN-96.
DR	PDB:	2SEB:	28-JAN-96.
DR	PDB:	3SEB:	17-MAY-98.
DR	PDB:	4SEB:	15-OCT-97.
DR	PDB:	1SEB:	04-MAR-99.
DR	InterPro:	IPR001961:	Stap/strep.toxin.
DR	Pfam:	PF02876:	Stap_strep_toxin_1.
DR	PRINTS:	PS00279:	BACTR/TOXIN.
DR	PROSITE:	PS00277:	STAPH_STREP_TOXIN_1.1.
DR	PROSITE:	PS00278:	STAPH_STREP_TOXIN_2.1.
DR	PROSITE:	PS00279:	STAPH_STREP_TOXIN_2.1.
DR	Stoichiometry:	toxin:	2(gmol), Superantigen: 3D-structure.
DR	Stoichiometry:	toxin:	2(gmol), Superantigen: 3D-structure.
DR	CHAIN:		
DR	DISULFID	120	140
DR	CONFLICT	56	58
DR	CONFLICT	69	77
DR	CONFLICT	118	118
DR	CONFLICT	128	130
DR	CONFLICT	138	140
DR	CONFLICT	149	150
DR	CONFLICT	156	156
DR	CONFLICT	185	185
DR	CONFLICT	233	233
DR	CONFLICT	246	247
DR	SEQUENCE	266 AA:	31135 MW: B6D11P6C101880 CR064;

Query Match	Score	DB 1	Length
Best Local Similarity	43.6%	Score 576.5	DB 1
Matches 133	Conservative	38	Mismatches 75
		Indels	19
		Gaps	7

  

DB	Accession	Score	DB 1	Length
DB	15 VYVTLGLTGIS-QGPEA--000PDSQLHSSLVKRL-QNITFLYEGDPYTHSNKSDQ	70		
DB	11 ILTFLPGLTISPPVLAASDPDRDELHNSKSTFLGKNDKMLSDVGNKKNKYLSDQ	70		
DB	71 LSHNOLLYANSP--NFDKLTFLKKNQDMATFLKDNKNVDIGVEYHNLFLYCENAA---	133		
DB	71 FLVFLFDLISKDTLVNDVAVREKFKMDLADYKDYKDYVFGANYYCYCKSKKNDIN	130		
DB	124-----EASACITGCVTHNBSNHLIEPKATIKVYSIDGJOSLSPDIEETKAKMTVAOELDK	178		
DB	131 SHDTKRNCKMCGVTEHKNQNDLDRVSTRVAFEDKMLNSLDVGNKKNKYLSDQ	130		
DB	179 VRYVLYLQKLTATMGSGSYETGYIKFLPKNKSEAFNFPDEPP--ETGSSYLYIKKNET	236		
DB	191 TRHYLVNKKKLTIEENNSYETGYIKFL--ENNSFVYDMPAPDKDFDSKXYLYMNDNM	249		
DB	237 LBSNTSGSLIEVLYTK	251		
DB	250 VDSKDYVNLIEVLYTK	264		

  

DB	Accession	Score	DB 1	Length
DB	15 VYVTLGLTGIS-QGPEA--000PDSQLHSSLVKRL-QNITFLYEGDPYTHSNKSDQ	70		
DB	11 ILTFLPGLTISPPVLAASDPDRDELHNSKSTFLGKNDKMLSDVGNKKNKYLSDQ	70		
DB	71 LSHNOLLYANSP--NFDKLTFLKKNQDMATFLKDNKNVDIGVEYHNLFLYCENAA---	133		
DB	71 FLVFLFDLISKDTLVNDVAVREKFKMDLADYKDYKDYVFGANYYCYCKSKKNDIN	130		
DB	124-----EASACITGCVTHNBSNHLIEPKATIKVYSIDGJOSLSPDIEETKAKMTVAOELDK	178		
DB	131 SHDTKRNCKMCGVTEHKNQNDLDRVSTRVAFEDKMLNSLDVGNKKNKYLSDQ	130		
DB	179 VRYVLYLQKLTATMGSGSYETGYIKFLPKNKSEAFNFPDEPP--ETGSSYLYIKKNET	236		
DB	191 TRHYLVNKKKLTIEENNSYETGYIKFL--ENNSFVYDMPAPDKDFDSKXYLYMNDNM	249		
DB	237 LBSNTSGSLIEVLYTK	251		
DB	250 VDSKDYVNLIEVLYTK	264		

  

DB	Accession	Score	DB 1	Length
DB	15 VYVTLGLTGIS-QGPEA--000PDSQLHSSLVKRL-QNITFLYEGDPYTHSNKSDQ	70		
DB	11 ILTFLPGLTISPPVLAASDPDRDELHNSKSTFLGKNDKMLSDVGNKKNKYLSDQ	70		
DB	71 LSHNOLLYANSP--NFDKLTFLKKNQDMATFLKDNKNVDIGVEYHNLFLYCENAA---	133		
DB	71 FLVFLFDLISKDTLVNDVAVREKFKMDLADYKDYKDYVFGANYYCYCKSKKNDIN	130		
DB	124-----EASACITGCVTHNBSNHLIEPKATIKVYSIDGJOSLSPDIEETKAKMTVAOELDK	178		
DB	131 SHDTKRNCKMCGVTEHKNQNDLDRVSTRVAFEDKMLNSLDVGNKKNKYLSDQ	130		
DB	179 VRYVLYLQKLTATMGSGSYETGYIKFLPKNKSEAFNFPDEPP--ETGSSYLYIKKNET	236		
DB	191 TRHYLVNKKKLTIEENNSYETGYIKFL--ENNSFVYDMPAPDKDFDSKXYLYMNDNM	249		
DB	237 LBSNTSGSLIEVLYTK	251		
DB	250 VDSKDYVNLIEVLYTK	264		

  

DB	Accession	Score	DB 1	Length
DB	15 VYVTLGLTGIS-QGPEA--000PDSQLHSSLVKRL-QNITFLYEGDPYTHSNKSDQ	70		
DB	11 ILTFLPGLTISPPVLAASDPDRDELHNSKSTFLGKNDKMLSDVGNKKNKYLSDQ	70		
DB	71 LSHNOLLYANSP--NFDKLTFLKKNQDMATFLKDNKNVDIGVEYHNLFLYCENAA---	133		
DB	71 FLVFLFDLISKDTLVNDVAVREKFKMDLADYKDYKDYVFGANYYCYCKSKKNDIN	130		
DB	124-----EASACITGCVTHNBSNHLIEPKATIKVYSIDGJOSLSPDIEETKAKMTVAOELDK	178		
DB	131 SHDTKRNCKMCGVTEHKNQNDLDRVSTRVAFEDKMLNSLDVGNKKNKYLSDQ	130		
DB	179 VRYVLYLQKLTATMGSGSYETGYIKFLPKNKSEAFNFPDEPP--ETGSSYLYIKKNET	236		
DB	191 TRHYLVNKKKLTIEENNSYETGYIKFL--ENNSFVYDMPAPDKDFDSKXYLYMNDNM	249		
DB	237 LBSNTSGSLIEVLYTK	251		
DB	250 VDSKDYVNLIEVLYTK	264		

  

DB	Accession	Score	DB 1	Length
DB	15 VYVTLGLTGIS-QGPEA--000PDSQLHSSLVKRL-QNITFLYEGDPYTHSNKSDQ	70		
DB	11 ILTFLPGLTISPPVLAASDPDRDELHNSKSTFLGKNDKMLSDVGNKKNKYLSDQ	70		
DB	71 LSHNOLLYANSP--NFDKLTFLKKNQDMATFLKDNKNVDIGVEYHNLFLYCENAA---	133		
DB	71 FLVFLFDLISKDTLVNDVAVREKFKMDLADYKDYKDYVFGANYYCYCKSKKNDIN	130		
DB	124-----EASACITGCVTHNBSNHLIEPKATIKVYSIDGJOSLSPDIEETKAKMTVAOELDK	178		
DB	131 SHDTKRNCKMCGVTEHKNQNDLDRVSTRVAFEDKMLNSLDVGNKKNKYLSDQ	130		
DB	179 VRYVLYLQKLTATMGSGSYETGYIKFLPKNKSEAFNFPDEPP--ETGSSYLYIKKNET	236		
DB	191 TRHYLVNKKKLTIEENNSYETGYIKFL--ENNSFVYDMPAPDKDFDSKXYLYMNDNM	249		
DB	237 LBSNTSGSLIEVLYTK	251		
DB	250 VDSKDYVNLIEVLYTK	264		

  

||
||
||

RA Kuroda N, Ohta T, Uchiyama I., Baba T, Yuzawa H, Kobayashi I.,  
RA Chi I., Oguchi A., Aoki K.-I., Nagai Y., Iisan J.-O., Ito T.,  
RA Kanomori M., Matsumaru H., Maruyama M., Wurokami H., Hosoyama A.,  
RA Mizutani-Oi Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
RA Sekimizu K., Hirakawa H., Kishida S., Goto S., Yabuzaki S.,  
RA Kamakura M., Yamashita A., Ohshima K., Furuya K., Yoshino C., Shiba T.,  
RA Hattori M., Ogasawara N., Hayashi R., Hiramatsu K.,  
RA Nakamura M., Genome sequencing of methicillin-resistant *Staphylococcus*  
RT aureus  
RT Lancet 357:1225-1240(2001).  
RL (2)  
RL  
RL  
RL  
RL  
RP SEQUENCE FROM N.A.  
RP MEDLINE-90220508; PubMed-2325627;  
RX Hovde C.J., Hackett S.P., Bonach G.A.;  
RX Nucleotide sequence of the staphylococcal enterotoxin G3 gene:  
RT sequence comparison of all three type C staphylococcal  
RT Mol. Gen. Genet. 220:339-333(1990).  
RL (3)  
RL  
RL X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.  
RX MEDLINE-97064178; PubMed-89056797;  
RX Fields B.A., Nalchodji E.L., Li H., Yaern X., Steaflacher C.V.,  
RX Schlievert P.M., Rajalathen R., Maritzza R.A.;  
RT Crystal structure of a T-cell receptor beta-chain complexed with a  
RT Nature 384:1180-1192(1996).  
CC -1- SUBCELLULAR LOCATION: secreted.  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.

[illegible]







```

RF enterotoxin D.*.
RF J. Bacteriol. 171:4795-4806(1989).
RN SEQUENCE FROM N.A. AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA STRAIN-ATCC 23235. PubMed-9003758.
RX Sundstrom M., Abrahamson L., Andersson P., Melinade K., Mourad W.,
  Dahlsten M.,
  "The crystal structure of staphylococcal enterotoxin type D reveals
  a 242-mediated homodimerization."
CC MEDLINE-90326840(1996).
CC PubMed-90326840(1996).
CC -1- SUBUNIT-DEPENDENT.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
  STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
  FAMILY.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation
  at the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@sib-sib.ch).
CC EMBL: M29531; AAB06195.1; -.
CC PIR: A33953; A33953.
CC HSSP: P13163; 1SMT.
CC InterPro: IPR001961; Strep/Strep_toxin.
CC Pfam: PF02876; Strep_toxin; 1.
CC PRINTS: PR00279; BACTSTREP_TOXIN; 1.
CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC Enterotoxin; Toxin; Signal; Superantigen; Zinc.
CC SIGNAL: 1 25
CC CHAIN: 1 25
CC METAL: 212 213
CC METAL: 250 250
CC METAL: 252 252
CC VARIANT: 114 114 P -> A (IN STRAIN ATCC 23235).
CC SEQUENCE: 258 AA; 29746 MW; 48FC6A2B842597ED CRC64.
Query Match
Best Local Similarity 35.78; Score 340; DB 1; Length 258;
Matches 92; Conservative 47; Mismatches 102; Indels 20; Gaps 10;
OY 8 LKMK-VFVLYVFLGLITLQ-EVFAQDDP--PSQIHR---SGLVKNLONTYVLEVG 57
DB 1 MKKFNLLALFLPFLSVLPVLANENIDVKEVLRKRSLSLALNMHSGY-ADK 58
OY 58 DPYTHNYSVNDLASHDLIYN--VSGPNYDKLTELKNOMATLFPDCAVDITGVCEYH 114
DB 59 NFPIENKSTGDFLENTLLTKKFFDILFEDLLINFSKEMAHQFSSKNDVYVIRIS 118
OY 115 HLCYCENMERSAGITGVYTHNDSNHLSEIPKIVYKVSIDGIG-SLSD-ITKMKKMYA 172
DB 119 INCIQGE-IDNKATIGGVTPHNP--SYETGYTPFIPKMSFPPFPERPETSOKYLM 230
OY 173 QEDLYKRYKILDKMQLTYMCP--SYETGYTPFIPKMSFPPFPERPETSOKYLM 230
DB 178 QEDLYKRYKILDKMQLTYMCP--SYETGYTPFIPKMSFPPFPERPETSOKYLM 230
OY 231 YKQNETLDSNNTSOJEVYITTK 251
DB 238 YSKNNTLSTFHNHIDILYTK 258

```

```

DT 01-JAN-1990 (rel. 13 Created)
DT 01-JAN-1990 (rel. 13 Sequence update)
DT 15-JUN-2002 (rel. 41; Last annotation update)
DE Enterotoxin type E precursor (smf).
OS ENTE.
GN Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CC EMBL: X602180;
CC MEDLINE-96022987; PubMed-7552730.
CC STRAIN-M4B265.
CC STRAIN-98257005; PubMed-3384800.
CC Couch J.L., Solis M.P., Pletcher J., Sax M.;
  "Cloning and nucleotide sequence of the type E staphylococcal
  enterotoxin gene."
CC Bacteriol. 170:2594-2601(1988).
RN 12)
RP 3D-STRUCTURE MODELING.
RX MEDLINE-96022987; PubMed-7552730.
RX Swaminathan S., Furey W.P., Jr., Pletcher J., Sax M.;
  "Residues defining V beta specificity in staphylococcal
  enterotoxin."
CC Bacteriol. 161: 2160-686(1995).
CC -1- COFACTOR: Binds 1 zinc ion (20% abundant. The zinc ion is necessary
  for the toxin interaction with MHC class II (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
  STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
  FAMILY.
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation
  at the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (see http://www.isb-sib.ch/announce/
  or send an email to license@sib-sib.ch).
CC EMBL: M21319; AAA26617.1; -.
CC PIR: A28179; A28179.
CC HSSP: P13163; 1SMT.
CC InterPro: IPR001961; Strep/Strep_toxin.
CC Pfam: PF02876; Strep_toxin; 1.
CC PRINTS: PR00279; BACTSTREP_TOXIN.
CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc.
CC SIGNAL: 1 27
CC CHAIN: 1 27
CC METAL: 211 211
CC METAL: 249 249
CC METAL: 251 251
CC SEQUENCE: 257 AA; 29398 MW; 27EDBA497770C3 CRC64.
Query Match
Best Local Similarity 32.74; Score 308; DB 1; Length 257;
Matches 86; Conservative 49; Mismatches 98; Indels 30; Gaps 11;
OY 10 KAVFVLYVFLGLITL-----SQEVFAQDDPSPQIHRSSLVKNLONTYVLEVD 58
DB 2 KRAFLLFLPFLSVLPVLANENIDVKEVLRKRSLSLALNMHSGY-ADK 59
OY 59 DPYTHNYSVNDLASHDLIYN--VSGPNYDKLTELKNOMATLFPDCAVDITGVCEYH 115
DB 60 AIT-ENKESDQFLENTLLFKGFQTHPMTNLLVYKSDKANKYKGGKDYGAAYGV 118
OY 116 LCTYCENMERSAGITGVYTHNDSNHLSEIPKIVYKVSIDGIG-SLSD-ITKMKKMYA 173
DB 119 INCIQGE-IDNKATIGGVTPHNP--SYETGYTPFIPKMSFPPFPERPETSOKYLM 230
OY 231 YKQNETLDSNNTSOJEVYITTK 251
DB 238 YSKNNTLSTFHNHIDILYTK 258

```

QY 174 ELVDYKARYLTDNKQLYTNGP--SKYEYETGKIFRNKSKSWPDPFPEPEPTOSKY----227  
 DB 178 ELLDQARHYLHNGKGLYNSDEGKQVDELIVFHSSSGSYSDLPD----AGQSDPDL 233  
 QY 228 LMTYDNELTDSNTSQTLYLT 250  
 DB 234 LRTYDNKNTINSEMDHIDLYLT 256  
 RESULT 9  
 EXTRA\_STAM STANDARD; PRT: 257 AA.  
 ID EXTRA\_STAM  
 AC 013163; 1990 (Rel. 13. Created)  
 DT 01-JAN-1990 (Rel. 13. Last sequence update)  
 DT 15-JUN-2002 (Rel. 13. Last annotation update)  
 DE Enterotoxin type A precursor (SEA).  
 GN ENTA OR MW1889.  
 OS Staphylococcus aureus (strain MW2), and  
 OS Staphylococcus aureus.  
 CC Staphylococcus aureus; Bacillales; Staphylococcus.  
 CO MW2; EnTA156620, 1280;  
 ON MW2; EnTA156620, 1280;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MW2.  
 RA MEDLINE-220401717; PubMed-12044378;  
 RA Babbs T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,  
 RA Nagai Y., Iwama N., Asano K., Nishitani T., Kuroda H., Cui L.,  
 RA Yamamoto K., Hirumatsu K.,  
 RA "Genomic evidence of high virulence determinants of high virulence community-  
 RT acquired MRSA."?  
 RL Lancet 359:1819-1827(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-FRI37.  
 RA MEDLINE-80186832; PubMed-335483;  
 RA "Nucleotide sequence of the type A staphylococcal enterotoxin gene."?  
 RT J. Bacteriol. 170:34-41(1988).  
 RN [3]  
 RP SEQUENCE OF 25-257.  
 RA MEDLINE-87222833; PubMed-3584106;  
 RA Huang I.-Y., Hughes D.L., Bergdoll M.S., Schantz E.J.;  
 RA "Enterotoxin A of staphylococcal enterotoxin A."?  
 RT J. Biol. Chem. 262:7006-7013(1987).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RA MEDLINE-95354648; PubMed-7628131;  
 RA Schind E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T.,  
 RA Schlievert P.M., Ohlendorf D.H., Svensson A.,  
 RA "Crystal structure of the superantigen staphylococcal enterotoxin  
 RT A."?  
 RL EMBL J. 14:3252-3301(1995).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
 RA MEDLINE-97113025; PubMed-8943278;  
 RA Sundstrom M., Hallen D., Svensson A., Schind E., Dohlsten M.,  
 RA Aramainen L.;  
 RA "The crystal structure of staphylococcal enterotoxin type A with  
 RT Zn2+ bound: implications for major histocompatibility  
 RT complex class II binding."?  
 RL J. Biol. Chem. 271:32213-32216(1996).  
 RN [6]  
 RP 3D-STRUCTURE MODELING.  
 RA MEDLINE-96022987; PubMed-7552730;  
 RA Swaminathan S., Puri W.F., Jr., Fletcher J., Sax M.;  
 RA "Modeling the V beta specificity in staphylococcal  
 RT enterotoxins."?  
 RL Nat. Struct. Biol. 2:680-686(1995).  
 RN [7]  
 RP COMPARISON OF STRUCTURE OF SEA AND SECA.  
 RA MEDLINE-9734373; PubMed-9191070;  
 RA Schind E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;

RT "A structural and functional comparison of staphylococcal  
 RT enterotoxins A and C2 reveals remarkable similarity and  
 RT dissimilarity."?  
 RL J. Mol. Biol. 269:270-280(1997).  
 CC -1- COFACTOR: Binds a zinc ion per subunit. The zinc ion is necessary  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 CC -1- STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.  
 CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN  
 CC FAMILIES.  
 CC -----  
 CC THIS SMSS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed, usage by and for commercial  
 CC entities requires a license agreement (see <http://www.elsb-sib.ch/announce/>  
 CC or [elsb@elsb.ch](mailto:elsb@elsb.ch)).  
 CC -----  
 CC EMBL: AP004828; BAB95754.1; -  
 CC EMBL: M18970; AA2681.1; -  
 CC EMBL: A28664; A28664.  
 CC PIR: A29566; A29566.  
 CC PDB: 1ESF; 1I; 30J; 96.  
 CC PDB: 1SEA; 1S; 30J; 97.  
 CC PDB: 1XU; 1XU; 97.  
 CC Interpret: IP001961; Staph/Strep.toxin; 1.  
 CC Pfam: PF01123; Staph-Strep.toxin; 1.  
 CC Pfam: PF02876; Staph-Strep.toxin.  
 CC PRINTS: PR00279; BACTRTOXIN.  
 CC PROSITE: PS00277; STAPH-STREP\_TOXIN\_1; 1.  
 CC PROSITE: PS00278; STAPH-STREP\_TOXIN\_2; 1.  
 CC KEGG: 30-structure; Toxin, Signal, Superantigen, Metal-binding; ZINC;  
 CC 3D-structure; 1; 24  
 CC FT SIGNAL 25 257 ENTEROTOXIN TYPE A.  
 CC FT CHAIN 120 130  
 CC FT DISULFID 211 211 ZINC.  
 CC FT METAL 249 249 ZINC.  
 CC FT METAL 249 249 ZINC.  
 CC FT CONFLICT 242 242 T (IN REF. 3).  
 CC SEQUENCE 257 AA; 29669 MW; ADBP55CAFL1677 CRC64;  
 Query Match 33.2%; score 307; DB 1; length 257;  
 Best Local Similarity 30.9%; Pred. No. 1.8e-16;  
 Matches 80; Conservative 49; Mismatches 108; Indels 22; Gaps 7;  
 10 KAVFVYLTFLGLT-----SGYRQADPDPSQMSLSLVNOMVYVLEED 58  
 2 KRTAFLLFLIALTLTTPSYLWNSKSEETNEKDLKRSKSGTAL-GNLFQY--TYNE 58  
 QY 59 PTFHENVASVOLDSHDLIYV--VSPVYQKLTETLKNQENATLTKQKNQDYOVEVYH 115  
 DB 59 KATNEKESDHPLOHITLFFGFTDSWMDLVDVSDSDVQKTRKAKVDYCAVYQY 118  
 QY 116 LTYLCNKAESACVGTGYNMGECNLEITIKYVYSIDTSL--SDITRKQVWQ 173  
 DB 116 QY-AGCTNNTKMGVGTGLDNNRLTEEKVPINLMDKQNTVPLETVYTRKKNVYQ 177  
 QY 174 ELVDYKARYLTDNKQLYTNG--PSKYETGKIFRNKSKSWPDPFPEPEPTOSKYVLT 231  
 DB 178 ELLDQARHYLHNGKGLYNSDEGKQVDELIVFHSSSGSYSDLPDAGQSDPDL 237  
 QY 232 LMTYDNELTDSNTSQTLYLT 250  
 DB 238 LRTYDNKNTINSEMDHIDLYLT 256  
 RESULT 10  
 SPCL\_STRIP

ID SPEC\_STRPY STANDARD: PRT: 235 AA.  
 AC PJ3380;  
 DT 01-JAN-1990 (rel. 13, Created)  
 DT 15-OCT-2001 (rel. 40, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Exotoxin type 1, 2, 1.  
 GN Exotoxin type 1 precursor (SPE C).  
 OS SPEC OR SP70711  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.  
 NC NCBI\_TaxID:1314;  
 NC SEQUENCE FROM N.A. AND SEQUENCE OF 28-52.  
 RC STRAIN-118P / MGAS\_1585;  
 RA MEDLINE-88314303; PubMed-3045005;  
 RX Goshorn S.C., Schlievert P.M.;  
 RT Nucleotide sequence of streptococcal pyrogenic exotoxin type C.  
 RT Infect. Immun. 56:2518-2520(1988).  
 RP REVIEWS TO 21-26.  
 RC STRAIN-118P / MGAS\_1585;  
 RA MEDLINE-92353441; PubMed-1500157;  
 RX Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;  
 RT Molecular population genetic evidence of horizontal spread of two alleles of the pyrogenic exotoxin C gene (speC) among pathogenic strains of Streptococcus pyogenes.  
 RT Infect. Immun. 60:3513-3517(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SF370 / ATCC\_700294 / Serotype M1;  
 RA MEDLINE-9132684; PubMed-11296596;  
 RX Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 RA Heape S.K., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
 RA Qian Y., Clifton S.W., Roe B.A., McCluskey H., Song L., White J.,  
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
 RN [4]  
 RP X-CRY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.  
 RX MEDLINE-93707353; PubMed-11965823;  
 RA Roumel A., Anderson B.P., Baker H.M., Fraser J.D., Baker E.N.;  
 RT Crystal structure of the streptococcal superantigen spe-C: dimerization and zinc binding suggest a novel mode of interaction with MHC class II molecules.  
 RT Nat. Struct. Biol. 4:635-643(1997).  
 RN [5]  
 RP SHIMMITS: Binds to major histocompatibility complex class II beta chain.  
 RT -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE THE CAUSATIVE AGENTS OF THE SYNDROME ASSOCIATED WITH SCARLET FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC FEVER.  
 RT -1- STRAIN: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way misused. The statement is not removed, usage by and for commercial entities requires statement (see http://www.isb-sb.ch/announce/ or send an email to license@isb-sb.ch)  
 CC EMBL: M35514; AAA7017.1; ALT\_SEO.  
 DR EMBL: M97156; AAB59091.1;  
 DR EMBL: M97157; AAB59092.1;  
 DR EMBL: M3006523; AAK33664.1;  
 DR EMBL: A30559;  
 DR PDB: 1AN9; 29-APR-98.  
 DR InterPro: IPR001961; stp/strep toxin.  
 DR Pfam: PF01123; Strep\_strp\_toxin1.1.

DR PFAM: PF02876; Strep\_strp\_tox\_C.1.  
 DR PRINTS: PR00279; BACTERIOTOXIN.  
 DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1.1.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2.1.  
 DR Toxin; Signal: 3D-structure; Complete proteome.  
 FT SIGNAL: 27  
 FT CHAIN: 28  
 FT CDS: 25  
 FT PROPEP: 33  
 FT SEQUENCE: 235 AA; 27971 MW; 07034AB852C1ED CMC64;  
 Query Match 16.3%; Score 215; DB 1; Length 235;  
 Best Local Similarity 28.2%; Pred. No. 1,5e-09;  
 Matches 72; Conservative 51; Mismatches 98; Indels 34; Gaps 12;  
 5 KYLVKAVFVVLPLGLTIGSEVFAQDDPSPGLHRSVLKMNQITLYEGDPVTHN 64  
 2 KININIVITFIVTLISTSP1IKSDKMDISNK-----SDLLKIVITPVDAIN 53  
 65 VNSVQALSHDLIYNSGPRVD---KLKTELKNOEMALFKRNANVDIGVEYHLCYL 120  
 34 CR-VFSPTRHL-NIDQKVRGHDYVLSBSSYASQKPFKRDHVPGL-FYIL--- 105  
 DY ENRSEKSGYGVGT---NHCNRIELFKPIKYSIDG--1GSLSPDIEFKMAYTADQL 175  
 121 ENRSEKSGYGVGT---NHCNRIELFKPIKYSIDG--1GSLSPDIEFKMAYTADQL 175  
 DB 106 -NSHGEYVGLSTPQAKNNVNH---KLGLNLFISGSQGLNNKMLLEKDIYVFEI 159  
 176 DYVVKYLTQKQVLTNPSEKVEGYIKFIPKNSKSPFDPPEP-FTQSKYLYMIDRN 234  
 160 DFKINKLMDNKIKT-DKTSIPVSGHTEIGTGKMGHEDLFLDPSFNGCTRSDIPAKYRDN 218  
 DB 235 ETLID-SNTSLELYTL 248  
 DB 219 RIINKNFSHDIYTL 233  
 RESULT 11  
 ID SPEC\_STRPY STANDARD: PRT: 236 AA.  
 AC 09X5C8;  
 DT 16-OCT-2001 (rel. 40, Created).  
 DT 15-OCT-2001 (rel. 40, Last sequence update)  
 DT 15-JUN-2002 (rel. 41, Last annotation update)  
 DE Exotoxin type 1, 2, 1.  
 GN Exotoxin type 1 precursor (SPE H).  
 OS SPEC OR SP7068  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.  
 NC NCBI\_TaxID:1314;  
 NC SEQUENCE FROM N.A.  
 RC STRAIN-118P / MGAS\_1585;  
 RA MEDLINE-21192684; PubMed-11296596;  
 RX Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,  
 RA Heape S.K., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
 RA Qian Y., Clifton S.W., Roe B.A., McCluskey H., Song L., White J.,  
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."  
 RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
 RN [5]  
 RP SHIMMITS: Binds to major histocompatibility complex class II beta chain.  
 RT -1- DISEASE: MITOGENIC FOR HUMAN PERIPHERAL BLOOD LYMPHOCYTES.  
 RT -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way misused. The statement is not removed, usage by and for commercial entities requires statement (see http://www.isb-sb.ch/announce/ or send an email to license@isb-sb.ch)  
 CC EMBL: M35514; AAA7017.1; ALT\_SEO.  
 DR EMBL: M97156; AAB59091.1;  
 DR EMBL: M97157; AAB59092.1;  
 DR EMBL: M3006523; AAK33664.1;  
 DR EMBL: A30559;  
 DR PDB: 1AN9; 29-APR-98.  
 DR InterPro: IPR001961; stp/strep toxin.  
 DR Pfam: PF01123; Strep\_strp\_toxin1.1.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is always by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/> or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).

EMBL: AF124500; AAC0989.1; -  
 EMBL: AE006489; AKK3307.1; -  
 DR HSPD: P13380.1; Step/strep toxin.  
 DR Interpro: IPR01361; Step/strep toxin.  
 DR Pfam: PF02876; Step.strep.toxC.1.  
 DR PRINTS: PS00277; STAPH\_STREP\_TOXIN.1; FALSE\_NEG.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN.2; 1.  
 DR Toxin: Signal; Complete proteome.  
 FT CHAIN 33 232 POTENTIAL TYPE H.  
 FT SEQUENCE 236 AA; 27485 MW; 1032232907AD40D CRC64;  
 Query Match 16.1%; Score 212.5; DB 1; Length 236;  
 Best Local Similarity 29.3%; Pred. No. 2.4e-09;  
 Matches 72; Conservative 38; Mismatches 113; Indels 23; Gaps 9;  
 Oy 8 LKKKFFVYVYFGLITISGVPAACQDPDSQALSHSVKNAITFYEEQDPYHNNKS 67  
 Db 10 LDKRYSMTLSFLTSVNVQNVNVTNRHNEISLYHDSN--LLKDSIKK--S 62  
 Oy 68 VQQLSHDLINVSQPNYDKLKTENQEMATLEKDKNDIYGEVYHCTYCENAKERS 127  
 Db 63 PDLVSHMLKTSVKRN--LSVEFKMDSIEFRKREVDVALSAQECV--CPKRRER 118  
 Oy 128 CLYGV--TNHEGNETLRKRIYKYSIDIGSLSDFENKKNMAGDELYKRYID 185  
 Db 119 --FGSLTINSEKKEIKVP---VWVCKSKQPPETIVKPKYTAQGVQIVAKLIK 172  
 Oy 186 NKQLYTNQPSKYETGTFPIPKNKESEWFD--FFPEPEFQSKYMLYNDENLISNQ 243  
 Db 173 KYDIINRQKQYTKGTYTDLNSGKQIVFDLYFGQND--NSMLKITSNNERIDTQPH 230  
 Oy 244 IEVLT 249  
 Db 231 VVVIS 236  
 RESULT 12  
 SPBG STRPY STANDARD: PRT; 234 AA.  
 AC Q9X5C7;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 GN SPBG OF ST0215 precursor (SPE G).  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI:Taxid-114;  
 OX 111  
 OX 112  
 OX 113  
 OX 114  
 OX 115  
 OX 116  
 OX 117  
 OX 118  
 OX 119  
 OX 120  
 OX 121  
 OX 122  
 OX 123  
 OX 124  
 OX 125  
 OX 126  
 OX 127  
 OX 128  
 OX 129  
 OX 130  
 OX 131  
 OX 132  
 OX 133  
 OX 134  
 OX 135  
 OX 136  
 OX 137  
 OX 138  
 OX 139  
 OX 140  
 OX 141  
 OX 142  
 OX 143  
 OX 144  
 OX 145  
 OX 146  
 OX 147  
 OX 148  
 OX 149  
 OX 150  
 OX 151  
 OX 152  
 OX 153  
 OX 154  
 OX 155  
 OX 156  
 OX 157  
 OX 158  
 OX 159  
 OX 160  
 OX 161  
 OX 162  
 OX 163  
 OX 164  
 OX 165  
 OX 166  
 OX 167  
 OX 168  
 OX 169  
 OX 170  
 OX 171  
 OX 172  
 OX 173  
 OX 174  
 OX 175  
 OX 176  
 OX 177  
 OX 178  
 OX 179  
 OX 180  
 OX 181  
 OX 182  
 OX 183  
 OX 184  
 OX 185  
 OX 186  
 OX 187  
 OX 188  
 OX 189  
 OX 190  
 OX 191  
 OX 192  
 OX 193  
 OX 194  
 OX 195  
 OX 196  
 OX 197  
 OX 198  
 OX 199  
 OX 200  
 OX 201  
 OX 202  
 OX 203  
 OX 204  
 OX 205  
 OX 206  
 OX 207  
 OX 208  
 OX 209  
 OX 210  
 OX 211  
 OX 212  
 OX 213  
 OX 214  
 OX 215  
 OX 216  
 OX 217  
 OX 218  
 OX 219  
 OX 220  
 OX 221  
 OX 222  
 OX 223  
 OX 224  
 OX 225  
 OX 226  
 OX 227  
 OX 228  
 OX 229  
 OX 230  
 OX 231  
 OX 232  
 OX 233  
 OX 234  
 OX 235  
 OX 236  
 OX 237  
 OX 238  
 OX 239  
 OX 240  
 OX 241  
 OX 242  
 OX 243  
 OX 244  
 OX 245  
 OX 246  
 OX 247  
 OX 248  
 OX 249  
 OX 250  
 OX 251  
 OX 252  
 OX 253  
 OX 254  
 OX 255  
 OX 256  
 OX 257  
 OX 258  
 OX 259  
 OX 260  
 OX 261  
 OX 262  
 OX 263  
 OX 264  
 OX 265  
 OX 266  
 OX 267  
 OX 268  
 OX 269  
 OX 270  
 OX 271  
 OX 272  
 OX 273  
 OX 274  
 OX 275  
 OX 276  
 OX 277  
 OX 278  
 OX 279  
 OX 280  
 OX 281  
 OX 282  
 OX 283  
 OX 284  
 OX 285  
 OX 286  
 OX 287  
 OX 288  
 OX 289  
 OX 290  
 OX 291  
 OX 292  
 OX 293  
 OX 294  
 OX 295  
 OX 296  
 OX 297  
 OX 298  
 OX 299  
 OX 300  
 OX 301  
 OX 302  
 OX 303  
 OX 304  
 OX 305  
 OX 306  
 OX 307  
 OX 308  
 OX 309  
 OX 310  
 OX 311  
 OX 312  
 OX 313  
 OX 314  
 OX 315  
 OX 316  
 OX 317  
 OX 318  
 OX 319  
 OX 320  
 OX 321  
 OX 322  
 OX 323  
 OX 324  
 OX 325  
 OX 326  
 OX 327  
 OX 328  
 OX 329  
 OX 330  
 OX 331  
 OX 332  
 OX 333  
 OX 334  
 OX 335  
 OX 336  
 OX 337  
 OX 338  
 OX 339  
 OX 340  
 OX 341  
 OX 342  
 OX 343  
 OX 344  
 OX 345  
 OX 346  
 OX 347  
 OX 348  
 OX 349  
 OX 350  
 OX 351  
 OX 352  
 OX 353  
 OX 354  
 OX 355  
 OX 356  
 OX 357  
 OX 358  
 OX 359  
 OX 360  
 OX 361  
 OX 362  
 OX 363  
 OX 364  
 OX 365  
 OX 366  
 OX 367  
 OX 368  
 OX 369  
 OX 370  
 OX 371  
 OX 372  
 OX 373  
 OX 374  
 OX 375  
 OX 376  
 OX 377  
 OX 378  
 OX 379  
 OX 380  
 OX 381  
 OX 382  
 OX 383  
 OX 384  
 OX 385  
 OX 386  
 OX 387  
 OX 388  
 OX 389  
 OX 390  
 OX 391  
 OX 392  
 OX 393  
 OX 394  
 OX 395  
 OX 396  
 OX 397  
 OX 398  
 OX 399  
 OX 400  
 OX 401  
 OX 402  
 OX 403  
 OX 404  
 OX 405  
 OX 406  
 OX 407  
 OX 408  
 OX 409  
 OX 410  
 OX 411  
 OX 412  
 OX 413  
 OX 414  
 OX 415  
 OX 416  
 OX 417  
 OX 418  
 OX 419  
 OX 420  
 OX 421  
 OX 422  
 OX 423  
 OX 424  
 OX 425  
 OX 426  
 OX 427  
 OX 428  
 OX 429  
 OX 430  
 OX 431  
 OX 432  
 OX 433  
 OX 434  
 OX 435  
 OX 436  
 OX 437  
 OX 438  
 OX 439  
 OX 440  
 OX 441  
 OX 442  
 OX 443  
 OX 444  
 OX 445  
 OX 446  
 OX 447  
 OX 448  
 OX 449  
 OX 450  
 OX 451  
 OX 452  
 OX 453  
 OX 454  
 OX 455  
 OX 456  
 OX 457  
 OX 458  
 OX 459  
 OX 460  
 OX 461  
 OX 462  
 OX 463  
 OX 464  
 OX 465  
 OX 466  
 OX 467  
 OX 468  
 OX 469  
 OX 470  
 OX 471  
 OX 472  
 OX 473  
 OX 474  
 OX 475  
 OX 476  
 OX 477  
 OX 478  
 OX 479  
 OX 480  
 OX 481  
 OX 482  
 OX 483  
 OX 484  
 OX 485  
 OX 486  
 OX 487  
 OX 488  
 OX 489  
 OX 490  
 OX 491  
 OX 492  
 OX 493  
 OX 494  
 OX 495  
 OX 496  
 OX 497  
 OX 498  
 OX 499  
 OX 500  
 OX 501  
 OX 502  
 OX 503  
 OX 504  
 OX 505  
 OX 506  
 OX 507  
 OX 508  
 OX 509  
 OX 510  
 OX 511  
 OX 512  
 OX 513  
 OX 514  
 OX 515  
 OX 516  
 OX 517  
 OX 518  
 OX 519  
 OX 520  
 OX 521  
 OX 522  
 OX 523  
 OX 524  
 OX 525  
 OX 526  
 OX 527  
 OX 528  
 OX 529  
 OX 530  
 OX 531  
 OX 532  
 OX 533  
 OX 534  
 OX 535  
 OX 536  
 OX 537  
 OX 538  
 OX 539  
 OX 540  
 OX 541  
 OX 542  
 OX 543  
 OX 544  
 OX 545  
 OX 546  
 OX 547  
 OX 548  
 OX 549  
 OX 550  
 OX 551  
 OX 552  
 OX 553  
 OX 554  
 OX 555  
 OX 556  
 OX 557  
 OX 558  
 OX 559  
 OX 560  
 OX 561  
 OX 562  
 OX 563  
 OX 564  
 OX 565  
 OX 566  
 OX 567  
 OX 568  
 OX 569  
 OX 570  
 OX 571  
 OX 572  
 OX 573  
 OX 574  
 OX 575  
 OX 576  
 OX 577  
 OX 578  
 OX 579  
 OX 580  
 OX 581  
 OX 582  
 OX 583  
 OX 584  
 OX 585  
 OX 586  
 OX 587  
 OX 588  
 OX 589  
 OX 590  
 OX 591  
 OX 592  
 OX 593  
 OX 594  
 OX 595  
 OX 596  
 OX 597  
 OX 598  
 OX 599  
 OX 600  
 OX 601  
 OX 602  
 OX 603  
 OX 604  
 OX 605  
 OX 606  
 OX 607  
 OX 608  
 OX 609  
 OX 610  
 OX 611  
 OX 612  
 OX 613  
 OX 614  
 OX 615  
 OX 616  
 OX 617  
 OX 618  
 OX 619  
 OX 620  
 OX 621  
 OX 622  
 OX 623  
 OX 624  
 OX 625  
 OX 626  
 OX 627  
 OX 628  
 OX 629  
 OX 630  
 OX 631  
 OX 632  
 OX 633  
 OX 634  
 OX 635  
 OX 636  
 OX 637  
 OX 638  
 OX 639  
 OX 640  
 OX 641  
 OX 642  
 OX 643  
 OX 644  
 OX 645  
 OX 646  
 OX 647  
 OX 648  
 OX 649  
 OX 650  
 OX 651  
 OX 652  
 OX 653  
 OX 654  
 OX 655  
 OX 656  
 OX 657  
 OX 658  
 OX 659  
 OX 660  
 OX 661  
 OX 662  
 OX 663  
 OX 664  
 OX 665  
 OX 666  
 OX 667  
 OX 668  
 OX 669  
 OX 670  
 OX 671  
 OX 672  
 OX 673  
 OX 674  
 OX 675  
 OX 676  
 OX 677  
 OX 678  
 OX 679  
 OX 680  
 OX 681  
 OX 682  
 OX 683  
 OX 684  
 OX 685  
 OX 686  
 OX 687  
 OX 688  
 OX 689  
 OX 690  
 OX 691  
 OX 692  
 OX 693  
 OX 694  
 OX 695  
 OX 696  
 OX 697  
 OX 698  
 OX 699  
 OX 700  
 OX 701  
 OX 702  
 OX 703  
 OX 704  
 OX 705  
 OX 706  
 OX 707  
 OX 708  
 OX 709  
 OX 710  
 OX 711  
 OX 712  
 OX 713  
 OX 714  
 OX 715  
 OX 716  
 OX 717  
 OX 718  
 OX 719  
 OX 720  
 OX 721  
 OX 722  
 OX 723  
 OX 724  
 OX 725  
 OX 726  
 OX 727  
 OX 728  
 OX 729  
 OX 730  
 OX 731  
 OX 732  
 OX 733  
 OX 734  
 OX 735  
 OX 736  
 OX 737  
 OX 738  
 OX 739  
 OX 740  
 OX 741  
 OX 742  
 OX 743  
 OX 744  
 OX 745  
 OX 746  
 OX 747  
 OX 748  
 OX 749  
 OX 750  
 OX 751  
 OX 752  
 OX 753  
 OX 754  
 OX 755  
 OX 756  
 OX 757  
 OX 758  
 OX 759  
 OX 760  
 OX 761  
 OX 762  
 OX 763  
 OX 764  
 OX 765  
 OX 766  
 OX 767  
 OX 768  
 OX 769  
 OX 770  
 OX 771  
 OX 772  
 OX 773  
 OX 774  
 OX 775  
 OX 776  
 OX 777  
 OX 778  
 OX 779  
 OX 780  
 OX 781  
 OX 782  
 OX 783  
 OX 784  
 OX 785  
 OX 786  
 OX 787  
 OX 788  
 OX 789  
 OX 790  
 OX 791  
 OX 792  
 OX 793  
 OX 794  
 OX 795  
 OX 796  
 OX 797  
 OX 798  
 OX 799  
 OX 800  
 OX 801  
 OX 802  
 OX 803  
 OX 804  
 OX 805  
 OX 806  
 OX 807  
 OX 808  
 OX 809  
 OX 810  
 OX 811  
 OX 812  
 OX 813  
 OX 814  
 OX 815  
 OX 816  
 OX 817  
 OX 818  
 OX 819  
 OX 820  
 OX 821  
 OX 822  
 OX 823  
 OX 824  
 OX 825  
 OX 826  
 OX 827  
 OX 828  
 OX 829  
 OX 830  
 OX 831  
 OX 832  
 OX 833  
 OX 834  
 OX 835  
 OX 836  
 OX 837  
 OX 838  
 OX 839  
 OX 840  
 OX 841  
 OX 842  
 OX 843  
 OX 844  
 OX 845  
 OX 846  
 OX 847  
 OX 848  
 OX 849  
 OX 850  
 OX 851  
 OX 852  
 OX 853  
 OX 854  
 OX 855  
 OX 856  
 OX 857  
 OX 858  
 OX 859  
 OX 860  
 OX 861  
 OX 862  
 OX 863  
 OX 864  
 OX 865  
 OX 866  
 OX 867  
 OX 868  
 OX 869  
 OX 870  
 OX 871  
 OX 872  
 OX 873  
 OX 874  
 OX 875  
 OX 876  
 OX 877  
 OX 878  
 OX 879  
 OX 880  
 OX 881  
 OX 882  
 OX 883  
 OX 884  
 OX 885  
 OX 886  
 OX 887  
 OX 888  
 OX 889  
 OX 890  
 OX 891  
 OX 892  
 OX 893  
 OX 894  
 OX 895  
 OX 896  
 OX 897  
 OX 898  
 OX 899  
 OX 900  
 OX 901  
 OX 902  
 OX 903  
 OX 904  
 OX 905  
 OX 906  
 OX 907  
 OX 908  
 OX 909  
 OX 910  
 OX 911  
 OX 912  
 OX 913  
 OX 914  
 OX 915  
 OX 916  
 OX 917  
 OX 918  
 OX 919  
 OX 920  
 OX 921  
 OX 922  
 OX 923  
 OX 924  
 OX 925  
 OX 926  
 OX 927  
 OX 928  
 OX 929  
 OX 930  
 OX 931  
 OX 932  
 OX 933  
 OX 934  
 OX 935  
 OX 936  
 OX 937  
 OX 938  
 OX 939  
 OX 940  
 OX 941  
 OX 942  
 OX 943  
 OX 944  
 OX 945  
 OX 946  
 OX 947  
 OX 948  
 OX 949  
 OX 950  
 OX 951  
 OX 952  
 OX 953  
 OX 954  
 OX 955  
 OX 956  
 OX 957  
 OX 958  
 OX 959  
 OX 960  
 OX 961  
 OX 962  
 OX 963  
 OX 964  
 OX 965  
 OX 966  
 OX 967  
 OX 968  
 OX 969  
 OX 970  
 OX 971  
 OX 972  
 OX 973  
 OX 974  
 OX 975  
 OX 976  
 OX 977  
 OX 978  
 OX 979  
 OX 980  
 OX 981  
 OX 982  
 OX 983  
 OX 984  
 OX 985  
 OX 986  
 OX 987  
 OX 988  
 OX 989  
 OX 990  
 OX 991  
 OX 992  
 OX 993  
 OX 994  
 OX 995  
 OX 996  
 OX 997  
 OX 998  
 OX 999  
 OX 1000  
 OX 1001  
 OX 1002  
 OX 1003  
 OX 1004  
 OX 1005  
 OX 1006  
 OX 1007  
 OX 1008  
 OX 1009  
 OX 1010  
 OX 1011  
 OX 1012  
 OX 1013  
 OX 1014  
 OX 1015  
 OX 1016  
 OX 1017  
 OX 1018  
 OX 1019  
 OX 1020  
 OX 1021  
 OX 1022  
 OX 1023  
 OX 1024  
 OX 1025  
 OX 1026  
 OX 1027  
 OX 1028  
 OX 1029  
 OX 1030  
 OX 1031  
 OX 1032  
 OX 1033  
 OX 1034  
 OX 1035  
 OX 1036  
 OX 1037  
 OX 1038  
 OX 1039  
 OX 1040  
 OX 1041  
 OX 1042  
 OX 1043  
 OX 1044  
 OX 1045  
 OX 1046  
 OX 1047  
 OX 1048  
 OX 1049  
 OX 1050  
 OX 1051  
 OX 1052  
 OX 1053  
 OX 1054  
 OX 1055  
 OX 1056  
 OX 1057  
 OX 1058  
 OX 1059  
 OX 1060  
 OX 1061  
 OX 1062  
 OX 1063  
 OX 1064  
 OX 1065  
 OX 1066  
 OX 1067  
 OX 1068  
 OX 1069  
 OX 1070  
 OX 1071  
 OX 1072  
 OX 1073  
 OX 1074  
 OX 1075  
 OX 1076  
 OX 1077  
 OX 1078  
 OX 1079  
 OX 1080  
 OX 1081  
 OX 1082  
 OX 1083  
 OX 1084  
 OX 1085  
 OX 1086  
 OX 1087  
 OX 1088  
 OX 1089  
 OX 1090  
 OX 1091  
 OX 1092  
 OX 1093  
 OX 1094  
 OX 1095  
 OX 1096  
 OX 1097  
 OX 1098  
 OX 1099  
 OX 1100  
 OX 1101  
 OX 1102  
 OX 1103  
 OX 1104  
 OX 1105  
 OX 1106  
 OX 1107  
 OX 1108  
 OX 1109  
 OX 1110  
 OX 1111  
 OX 1112  
 OX 1113  
 OX 1114  
 OX 1115  
 OX 1116  
 OX 1117  
 OX 1118  
 OX 1119  
 OX 1120  
 OX 1121  
 OX 1122  
 OX 1123  
 OX 1124  
 OX 1125  
 OX 1126  
 OX 1127  
 OX 1128  
 OX 1129  
 OX 1130  
 OX 1131  
 OX 1132  
 OX 1133  
 OX 1134  
 OX 1135  
 OX 1136  
 OX 1137  
 OX 1138  
 OX 1139  
 OX 1140  
 OX 1141  
 OX 1142  
 OX 1143  
 OX 1144  
 OX 1145  
 OX 1146  
 OX 1147  
 OX 1148  
 OX 1149  
 OX 1150  
 OX 1151  
 OX 1152  
 OX 1153  
 OX 1154  
 OX 1155  
 OX 1156  
 OX 1157  
 OX 1158  
 OX 1159  
 OX 1160  
 OX 1161  
 OX 1162  
 OX 1163  
 OX 1164  
 OX 1165  
 OX 1166  
 OX 1167  
 OX 1168  
 OX 1169  
 OX 1170  
 OX 1171  
 OX 1172  
 OX 1173  
 OX 1174  
 OX 1175  
 OX 1176  
 OX 1177  
 OX 1178  
 OX 1179  
 OX 1180  
 OX 1181  
 OX 1182  
 OX 1183  
 OX 1184  
 OX 1185  
 OX 1186  
 OX 1187  
 OX 1188  
 OX 1189  
 OX 1190  
 OX 1191  
 OX 1192  
 OX 1193  
 OX 1194  
 OX 1195  
 OX 1196  
 OX 1197  
 OX 1198  
 OX 1199  
 OX 1200  
 OX 1201  
 OX 1202  
 OX 1203  
 OX 1204  
 OX 1205  
 OX 1206  
 OX 12





```

FT VANSPLIC 830 840 KYLCODEEH -> ESIRGHTLINK (IN ISOFORM
FT VANSPLIC 841 894 1B).
FT VANSPLIC 841 894 MISSING (IN ISOFORM 1B).
FT VANSPLIC 841 894 T->S (IN REF 3).
SQ SEQUENCE 894 AA; 100044 MW; 44BN35030893E3E1 CRC64;

Query Match 7.9%; Score 105; DB 1; Length 894;
Best Local Similarity 19.8%; Pred. No. 1.7;
Matches 51; Conservative 44; Mismatches 78; Indels 84; Gaps 10;

QY 34 PDPSQLHRSLLVNMKNITFLYEGDPYTHENKSVQDLKSHDLIYVSGPNYDKLTKELK 93
DB 138 PIAISMENSLGPPQHY-----QOIOS-DAQNVITITISISGCVDAKPFNL 185
QY 94 NQEMAT--LFKDKNDIYGEVYVHLYLCENADRSACIYGVTHGCHNLEIPKKIYAV 151
DB 186 YLEKTDGIDFCTRSDIREKYEQF-----ALYVATYADGYAPPEYPLPIIKI 232
QY 152 SIQGLSLSPDIE-----TNKNVTAQELD-----YVAKYLYDNKO 188
DB 233 EDONNAPVTEHRTITVPCNCRSGTSVGVATADLDLDEPDTLHLEKIKILQDIPNKK 292
QY 189 LYNQPSKYEYGYI--KFIQNKESFV-----PDPP----- 217
DB 293 HFSIHP--DTGVITTTYPFLDREKCPYOLIMEYVDMGQGFELNQTGITISLEDND 349
QY 218 PEPETQSKYLAIKDN 234
DB 350 NPSPFTETSYVTEVEN 366

```

Search completed: June 23, 2003, 16:13:00  
 Job time : 11.7747 secs





```

FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA: 27454 MW: 3763541ABDC13A84 CRC64:
Query Match 93.8%: Score 1240; DB 2; Length 236;
Best Local Similarity 99.6%: Pred. No. 4e-81; 1; Indels 0; Gaps 0;
Matches 235; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 KKNFVFLVTFGLGITSOEVFADDPDPSPQSHSSSLVKNLONTIPLYEGDPVTEHNVSV 68
DB 1 KKNFVFLVTFGLGITSOEVFADDPDPSPQSHSSSLVKNLONTIPLYEGDPVTEHNVSV 60
OY 69 DQLSHDLIYNSGPYDOKLTKELKNQEMATLEKDKNVDIYGVEYHLCYLENARSAC 128
DB 61 DQLSHDLIYNSGPYDOKLTKELKNQEMATLEKDKNVDIYGVEYHLCYLENARSAC 120
OY 129 IYGGVTHNBSNLEIKRKIVAVVSDIOSLSFDLETNKKWTAQOELDYVVKRLTDNKK 188
DB 121 IYGGVTHNBSNLEIKRKIVAVVSDIOSLSFDLETNKKWTAQOELDYVVKRLTDNKK 180
OY 189 LITNPSKRYETGYIKFKIRKKSFPDPPPEPTOSKLYMTYKDNETLDSNTSOI 244
DB 181 LITNPSKRYETGYIKFKIRKKSFPDPPPEPTOSKLYMTYKDNETLDSNTSOI 236

- RESULT 2
ID 054779 PRELIMINARY; PRF: 236 AA.
AC 054779: 054613: 054736: 054740: 054741:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DB Type A exotoxin precursor (Fragment).
OS Streptococcus pyogenes.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1314;
RN 1)
RP SEQUENCE FROM N.A.
RA PRINCE-9204323; PubMed-1940804; Nelson K., Sclavert P.M., Sclander R.K., Musser J.M.;
RA Characterization and clonal distribution of four alleles of the speA
RA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RA Streptococcus pyogenes.
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL: X61569: CAA43767.1; -
DR EMBL: X61564: CAA43765.1; -
DR EMBL: X61568: CAA43760.1; -
DR EMBL: X61570: CAA43768.1; -
DR EMBL: X61571: CAA43769.1; -
DR HSBP: P08095: 1B12.
DR Interpro: IPR001961; Strep/Strep-toxin.
DR Pfam: PF01123; Strep_Strep_toxin_1.
DR PRINTS: P080277; STAPH_STREP_TOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2.
KM signal.
FT NON_TER 1
FT SIGNAL 22
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA: 27469 MW: 20D72AD56523A84 CRC64:
Query Match 93.7%: Score 1239; DB 2; Length 236;
Best Local Similarity 99.2%: Pred. No. 4.7e-81;
Matches 234; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 KKNFVFLVTFGLGITSOEVFADDPDPSPQSHSSSLVKNLONTIPLYEGDPVTEHNVSV 68
DB 1 KKNFVFLVTFGLGITSOEVFADDPDPSPQSHSSSLVKNLONTIPLYEGDPVTEHNVSV 60
OY 69 DQLSHDLIYNSGPYDOKLTKELKNQEMATLEKDKNVDIYGVEYHLCYLENARSAC 128
DB 61 DQLSHDLIYNSGPYDOKLTKELKNQEMATLEKDKNVDIYGVEYHLCYLENARSAC 120
OY 129 IYGGVTHNBSNLEIKRKIVAVVSDIOSLSFDLETNKKWTAQOELDYVVKRLTDNKK 188
DB 121 IYGGVTHNBSNLEIKRKIVAVVSDIOSLSFDLETNKKWTAQOELDYVVKRLTDNKK 180
OY 189 LITNPSKRYETGYIKFKIRKKSFPDPPPEPTOSKLYMTYKDNETLDSNTSOI 244
DB 181 LITNPSKRYETGYIKFKIRKKSFPDPPPEPTOSKLYMTYKDNETLDSNTSOI 236

```

```

OY 69 DQLSHDLIYNSGPYDOKLTKELKNQEMATLEKDKNVDIYGVEYHLCYLENARSAC 128
DB 61 DQLSHDLIYNSGPYDOKLTKELKNQEMATLEKDKNVDIYGVEYHLCYLENARSAC 120
OY 129 IYGGVTHNBSNLEIKRKIVAVVSDIOSLSFDLETNKKWTAQOELDYVVKRLTDNKK 188
DB 121 IYGGVTHNBSNLEIKRKIVAVVSDIOSLSFDLETNKKWTAQOELDYVVKRLTDNKK 180
OY 189 LITNPSKRYETGYIKFKIRKKSFPDPPPEPTOSKLYMTYKDNETLDSNTSOI 244
DB 181 LITNPSKRYETGYIKFKIRKKSFPDPPPEPTOSKLYMTYKDNETLDSNTSOI 236

RESULT 3
ID 057453 PRELIMINARY; PRF: 236 AA.
AC 057453:
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DB Type A exotoxin precursor (Fragment).
GN SPEX.
OS Streptococcus pyogenes.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1314;
RN 1)
RP SEQUENCE FROM N.A.
RA MEDLINE-92044323; PubMed-1940804; Nelson K., Sclavert P.M., Sclander R.K., Musser J.M.;
RA Characterization and clonal distribution of four alleles of the speA
RA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RA Streptococcus pyogenes.
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL: X61563: CAA43760.1; -
DR EMBL: X61567: CAA43761.1; -
DR EMBL: X61569: CAA43765.1; -
DR EMBL: X61564: CAA43768.1; -
DR EMBL: X61568: CAA43762.1; -
DR EMBL: X61566: CAA43763.1; -
DR EMBL: X61565: CAA43764.1; -
DR HSBP: P08095: 1B12.
DR Interpro: IPR001961; Strep/Strep-toxin.
DR Pfam: PF01123; Strep_Strep_toxin_1.
DR PRINTS: P080277; STAPH_STREP_TOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2.
KM signal.
FT NON_TER 1
FT SIGNAL 22
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236
SQ SEQUENCE 236 AA: 27484 MW: 2E7F741AC853600 CRC64:
Query Match 93.3%: Score 1234; DB 2; Length 236;
Best Local Similarity 99.2%: Pred. No. 1.1e-80;
Matches 234; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 9 KKNFVFLVTFGLGITSOEVFADDPDPSPQSHSSSLVKNLONTIPLYEGDPVTEHNVSV 68
DB 1 KKNFVFLVTFGLGITSOEVFADDPDPSPQSHSSSLVKNLONTIPLYEGDPVTEHNVSV 60
OY 69 DQLSHDLIYNSGPYDOKLTKELKNQEMATLEKDKNVDIYGVEYHLCYLENARSAC 128
DB 61 DQLSHDLIYNSGPYDOKLTKELKNQEMATLEKDKNVDIYGVEYHLCYLENARSAC 120
OY 129 IYGGVTHNBSNLEIKRKIVAVVSDIOSLSFDLETNKKWTAQOELDYVVKRLTDNKK 188
DB 121 IYGGVTHNBSNLEIKRKIVAVVSDIOSLSFDLETNKKWTAQOELDYVVKRLTDNKK 180

```

```

OY 189 LVTNGSPKSYETGTYKIFPKNKESFWEFPEPEPTOSKLYMTKDNETLDSNTS01 244
    |||||||
DB 181 LVTNGSPKSYETGTYKIFPKNKESFWEFPEPEPTOSKLYMTKDNETLDSNTS01 236

RESULT 4
O98931 PRELIMINARY: PRT: 222 AA.
AC O98931 PRELIMINARY: 13, Created
DR 01-MAY-2000 (TREMblrel, 01, last annotation update)
DE 01-MAY-2000 (TREMblrel, 20, last annotation update)
DE Exotoxin A (fragment).
GN SPCA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
DR Streptococcaceae; Streptococcus.
CX NCBI_TaxID=1314;
RP SEQUENCE FROM N.A.
RC STRAIN-D709;
RA MEDLINE-99137798; PubMed-9952369;
RA Bessen D.E., Izzo M.M., Florentino T.R., Carlingal R.M.,
RA Hollingshead S.K., Beall B.;
RA Genetic linkage of exotoxin A alleles and emm gene markers for tissue
RA tropism in group A streptococci.
RA J Infect Dis 179:657-666(1999).
DR EMBL: AF056568; M611624.1; -.
DR HSPF: P08095; 181Z.
DR InterPro: IPR001961; Strep/Strep_toxin.
DR Pfam: PF01123; Strep_Strep_toxin_1.
DR Pfam: PF02876; Strep_Strep_toxin_1.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT SEQUENCE 222 AA; 23759 MW; 488B7ADCC091FBA3 CRC64;
SO QUERY MATCH 88.7%; Score 1173; DB 2; Length 222;
Best Local Similarity 99.5%; Pred. No. 2, 2e-76;
Matches 221; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 21 GUTISQVPAQDPSPQSLHRSLSVKNLQNTIFLYEGDPVTHENKSYQGLRSHDIYAN 80
    |||||||
DB 1 GUTISQVPAQDPSPQSLHRSLSVKNLQNTIFLYEGDPVTHENKSYQGLRSHDIYAN 60

OY 81 SGNDIDKLTETLNKQBATLFDKANDYDVEGYVLCYCENAESACTIGGVANEHGN 140
    |||||||
DB 61 SGNDIDKLTETLNKQBATLFDKANDYDVEGYVLCYCENAESACTIGGVANEHGN 120

OY 141 LEIPKIVVNSIDGIGLSFTIEKKNQVNOELDYVRYRTYTONKQXTGSGSYTCG 200
    |||||||
DB 121 LEIPKIVVNSIDGIGLSFTIEKKNQVNOELDYVRYRTYTONKQXTGSGSYTCG 180

OY 201 YKEFIPKNSFWEFPEPEPTOSKLYMTKDNETLDSNTS 242
    |||||||
DB 181 YKEFIPKNSFWEFPEPEPTOSKLYMTKDNETLDSNTS 222

RESULT 5
O54696 PRELIMINARY: PRT: 236 AA.
AC O54696 PRELIMINARY: 01, Created
DR 01-MAY-1996 (TREMblrel, 01, last annotation update)
DE 01-MAY-1996 (TREMblrel, 20, last annotation update)
DE Type A exotoxin precursor (fragment).
GN SPCA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
DR Streptococcaceae; Streptococcus.
CX NCBI_TaxID=1314;

```

```

RN 111
    |||||||
RX SEQUENCE FROM N.A.
RC STRAIN-WGAS156;
RA MEDLINE-92044323; PubMed-1940804;
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RA Characterization and clonal distribution of four toxin) in
RA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RA group A streptococci.
RA J Infect Med 174:1271-1274(1991).
DR EMBL: X61573; CAA43771.1; -.
DR HSPF: P08095; 181Z.
DR InterPro: IPR001961; Strep/Strep_toxin.
DR Pfam: PF01123; Strep_Strep_toxin_1.
DR Pfam: PF02876; Strep_Strep_toxin_1.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CRAIN 236 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SO SEQUENCE 236 AA; 27575 MW; 70E54120E79127DF CRC64;

QUERY MATCH 83.9%; Score 1109; DB 2; Length 236;
Best Local Similarity 86.6%; Pred. No. 8, 9e-72;
Matches 209; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

OY 9 KXMPVYVPGFATISQVPAQDPSPQSLHRSLSVKNLQNTIFLYEGDPVTHENKSV 68
    |||||||
DB 1 KXMPVYVPGFATISQVPAQDPSPQSLHRSLSVKNLQNTIFLYEGDPVTHENKSV 60

OY 69 DQLSHDIYANSGPNTDKLTETLNKQBATLFDKANDYDVEGYVLCYCENAESACT 120
    |||||||
DB 61 DQLSHDIYANSGPNTDKLTETLNKQBATLFDKANDYDVEGYVLCYCENAESACT 100

OY 129 YGGVTVNEGNHLEIPKIVVNSIDGIGLSFTIEKKNQVNOELDYVRYRTYTONKQ 188
    |||||||
DB 121 YGGVTVNEGNHLEIPKIVVNSIDGIGLSFTIEKKNQVNOELDYVRYRTYTONKQ 160

OY 189 LVTNGSPKSYETGTYKIFPKNKESFWEFPEPEPTOSKLYMTKDNETLDSNTS01 244
    |||||||
DB 181 LVTNGSPKSYETGTYKIFPKNKESFWEFPEPEPTOSKLYMTKDNETLDSNTS01 236

RESULT 6
O98524 PRELIMINARY: PRT: 222 AA.
AC O98524 PRELIMINARY: 13, Created
DR 01-MAY-2000 (TREMblrel, 01, last annotation update)
DE 01-MAY-2000 (TREMblrel, 20, last annotation update)
DE Exotoxin type A (fragment).
GN SPCA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
DR Streptococcaceae; Streptococcus.
CX NCBI_TaxID=1314;
RP SEQUENCE FROM N.A.
RC STRAIN-D633; PubMed-9952369;
RA Bessen D.E., Izzo M.M., Florentino T.R., Carlingal R.M.,
RA Hollingshead S.K., Beall B.;
RA Genetic linkage of exotoxin A alleles and emm gene markers for tissue
RA tropism in group A streptococci.
RA J Infect Dis 179:657-666(1999).
DR EMBL: AF056568; M611624.1; -.
DR HSPF: P08095; 181Z.
DR InterPro: IPR001961; Strep/Strep_toxin.
DR Pfam: PF01123; Strep_Strep_toxin_1.
DR Pfam: PF02876; Strep_Strep_toxin_1.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CRAIN 236 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SO SEQUENCE 236 AA; 27575 MW; 70E54120E79127DF CRC64;

```

DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 FT NON-TER 222  
 ST 1  
 SEQUENCE 222 AA; 25864 MW; 121F8460992818F8 CRC64;

Query Match 79.7%; Score 1054; DB 2; Length 222;  
 Best Local Similarity 89.2%; Pred. No. 76-68  
 Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

21 GLTISQVYVADQPPQSLAHSSLVKNLQNTYFLYEDGDPYVHNKMSVQQLSHDLIYV 80  
 1 GLTISQVYVADQPPQSLAHSSLVKNLQNTYFLYEDGDPYVHNKMSVQQLSHDLIYV 60  
 81 SGPNDKLTATLKNQEMATLFDKQVNDVYGVYHCTLCENAKRSACITGGYTHNCGH 140  
 1 SGPNDKLTATLKNQEMATLFDKQVNDVYGVYHCTLCENAKRSACITGGYTHNCGH 120  
 141 LELPKYLVKYSIDIOSLSPDIETSKKNTVYGVYHCTLCENAKRSACITGGYTHNCGH 180  
 121 LELPKYLVKYSIDIOSLSPDIETSKKNTVYGVYHCTLCENAKRSACITGGYTHNCGH 160  
 201 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 242  
 181 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 222

RESULT 7  
 ID 03678 PRELIMINARY; PR: 222 AA.  
 AC 093874  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Pyrogenic exotoxin A (fragment).  
 OS Streptococcus equi subsp. edwardsii  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 ST Streptococcaceae; Streptococcus.  
 NCBI\_TaxID=119602;  
 RX 11  
 RN SEQUENCE FROM N.A.  
 RA Kella A 1993; Beason D.E.;  
 RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human  
 RL isolated of group G Streptococcus."  
 RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.  
 EMBL; AF047945; AL00068.1; -  
 DR Genbank; F06001961; Step/Step-toxin.  
 DR Pfam; PF02876; Step-Step-toxin; 1.  
 DR Pfam; PF02876; Step-Step-toxin; 1.  
 DR PROSITE; PS00277; STAPH\_STREP\_TOXIN\_1; UNKNOWN; 1.  
 DR PROSITE; PS00278; STAPH\_STREP\_TOXIN\_2; UNKNOWN; 1.  
 FT NON-TER 222  
 ST 1  
 SEQUENCE 222 AA; 25864 MW; 121F8460992818F8 CRC64;

Query Match 79.7%; Score 1054; DB 2; Length 222;  
 Best Local Similarity 89.2%; Pred. No. 76-68  
 Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

21 GLTISQVYVADQPPQSLAHSSLVKNLQNTYFLYEDGDPYVHNKMSVQQLSHDLIYV 80  
 1 GLTISQVYVADQPPQSLAHSSLVKNLQNTYFLYEDGDPYVHNKMSVQQLSHDLIYV 60  
 81 SGPNDKLTATLKNQEMATLFDKQVNDVYGVYHCTLCENAKRSACITGGYTHNCGH 140  
 1 SGPNDKLTATLKNQEMATLFDKQVNDVYGVYHCTLCENAKRSACITGGYTHNCGH 120  
 141 LELPKYLVKYSIDIOSLSPDIETSKKNTVYGVYHCTLCENAKRSACITGGYTHNCGH 180  
 121 LELPKYLVKYSIDIOSLSPDIETSKKNTVYGVYHCTLCENAKRSACITGGYTHNCGH 160  
 201 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 242  
 181 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 222

OY 201 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 242  
 DB 181 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 222

Query Match 79.7%; Score 1054; DB 2; Length 222;  
 Best Local Similarity 89.2%; Pred. No. 76-68  
 Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

21 GLTISQVYVADQPPQSLAHSSLVKNLQNTYFLYEDGDPYVHNKMSVQQLSHDLIYV 80  
 1 GLTISQVYVADQPPQSLAHSSLVKNLQNTYFLYEDGDPYVHNKMSVQQLSHDLIYV 60  
 81 SGPNDKLTATLKNQEMATLFDKQVNDVYGVYHCTLCENAKRSACITGGYTHNCGH 140  
 1 SGPNDKLTATLKNQEMATLFDKQVNDVYGVYHCTLCENAKRSACITGGYTHNCGH 120  
 141 LELPKYLVKYSIDIOSLSPDIETSKKNTVYGVYHCTLCENAKRSACITGGYTHNCGH 180  
 121 LELPKYLVKYSIDIOSLSPDIETSKKNTVYGVYHCTLCENAKRSACITGGYTHNCGH 160  
 201 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 242  
 181 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 222

Query Match 79.7%; Score 1054; DB 2; Length 222;  
 Best Local Similarity 89.2%; Pred. No. 76-68  
 Matches 198; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

21 GLTISQVYVADQPPQSLAHSSLVKNLQNTYFLYEDGDPYVHNKMSVQQLSHDLIYV 80  
 1 GLTISQVYVADQPPQSLAHSSLVKNLQNTYFLYEDGDPYVHNKMSVQQLSHDLIYV 60  
 81 SGPNDKLTATLKNQEMATLFDKQVNDVYGVYHCTLCENAKRSACITGGYTHNCGH 140  
 1 SGPNDKLTATLKNQEMATLFDKQVNDVYGVYHCTLCENAKRSACITGGYTHNCGH 120  
 141 LELPKYLVKYSIDIOSLSPDIETSKKNTVYGVYHCTLCENAKRSACITGGYTHNCGH 180  
 121 LELPKYLVKYSIDIOSLSPDIETSKKNTVYGVYHCTLCENAKRSACITGGYTHNCGH 160  
 201 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 242  
 181 YKTKIPKNSKSEFMDFPEPEFOSKYLMATIKONETLDSNTS 222



DB 122 HFDNGNLQNVLYRVEENKRNITISFEVQDCKSVTAQOELDIKARNELINKNLYFENSFV 181  
 QY 198 ETGYIKETIPKNSFWEFFEPF--EFTOSKLYMTIYKDNELTSLNTSOIEVLTTK 231  
 DB 182 ETGYIKETIPKNSFWEFFEPF--EFTOSKLYMTIYKDNELTSLNTSOIEVLTTK 237

## RESULT 12

005157 PRELIMINARY: PRT: 239 AA.  
 ID 005157  
 AC 005157 (TREMBL:04. Created)  
 DT 01-JUL-1997 (TREMBL:04. Last annotation update)  
 DT 01-MAR-2002 (TREMBL:20. Last annotation update)  
 DE Type C enterotoxin (fragment).  
 OS Staphylococcus Intermedicus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Staphylococcus.  
 NC NCBI\_FtaxID=1280;  
 RP SEQUENCE FROM N.A.

RA Edwards V.M., Deringer J.R., Callentine S.D., Deobald C.F.,  
 RA Berger P.H., Kapur V., Stauffer C.V., Bohach G.A.;  
 RT Characterization of the type C enterotoxin (SEC-antigen) produced by  
 RT Staphylococcus Intermedicus proteome isolates.  
 RT J. Biol. Chem. 272:10132-10136 (1997).  
 DR EMBL: U01326; AA0246.1;  
 DR HSPF: P23131; ICKX.  
 DR Interpro: IPRO01961; Step/Step-toxin.  
 DR Pfam: PF01123; Step\_stp\_toxin; 1.  
 DR PRINTS: PR00279; BACSTRTOXIN.  
 DR PROSITE: PS00276; STAPH\_STREP\_TOXIN\_2; 1.  
 FT NON\_TER 1  
 FT SEQUENCE 239 AA; 27536 MW; D60644660EA191 CRC64;

Query Match 41.5%; Score 548; DB 2; Length 239;  
 Best Local Similarity 47.5%; Pred. No. 9.9e-32;

Matches 112; Conservative 42; Mismatches 68; Indels 14; Gaps 6;

QY 30 AADPPPSOLHRS--LYNKLNITLYLEEDDYVHEKNSYQDLSSIDLITVNSC---PY 85  
 DB 2 SDDPMPDHLHSESEPTGCKMKNCKLYDHYVATKRVSKVDFLAHDIYNISDKRKY 61  
 QY 86 DKLTETLNQEMATLFRKQNVDTGYEYVHLYTC--ENAE---SACTYGVYTHN 139  
 DB 62 DKRTLELNDAKRNKDEVDYGSNTVYCTFSKKNQVYGGCKTKHGLGTLNPSKY 121  
 QY 140 ELKEIP--KTIYVYSIDIGSLSPDIEKTKMTYAGELDYKRYKLYTNHQLYTNPSKY 197  
 DB 122 HFDNGNLQNVLYRVEENKRNITISFEVQDCKSVTAQOELDIKARNELINKNLYFENSFV 181  
 QY 198 ETGYIKETIPKNSFWEFFEPF--EFTOSKLYMTIYKDNELTSLNTSOIEVLTTK 231  
 DB 182 ETGYIKETIPKNSFWEFFEPF--EFTOSKLYMTIYKDNELTSLNTSOIEVLTTK 237

## RESULT 13

006531 PRELIMINARY: PRT: 239 AA.  
 ID 006531  
 AC 006531 (TREMBL:01. Created)  
 DT 01-NOV-1996 (TREMBL:01. Last annotation update)  
 DT 01-MAR-2002 (TREMBL:20. Last annotation update)  
 DE Enterotoxin type C-4 (SEC446) (Fragment).  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Staphylococcus.  
 NC NCBI\_FtaxID=1280;  
 RP SEQUENCE FROM N.A.

RC STRAIN=4446; PubMed=8406814;  
 RX MEDLINE=94011313; PubMed=8406814;  
 RA Marr J.C., Lyon J.D., Robertson J.R., Luper M., Bohach G.A.;  
 RT Characterization of novel type C staphylococcal enterotoxins:  
 RT Enterotoxin type C-4 (SEC446) (Fragment).  
 RT Infect Immun 61:4254-4262 (1993).  
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
 CC PYOGENIC EXOTOXINS ARE ALL RELATED.

DR EMBL: U01326; AA0246.1;  
 DR HSPF: P23131; ICKX.  
 DR Interpro: IPRO01961; Step/Step-toxin.  
 DR Pfam: PF01123; Step\_stp\_toxin; 1.  
 DR PRINTS: PR00279; BACSTRTOXIN.  
 DR PROSITE: PS00276; STAPH\_STREP\_TOXIN\_2; 1.  
 DR PROSITE: PS00276; STAPH\_STREP\_TOXIN\_2; 1.  
 NC NCBI\_FtaxID=1280;  
 RP SEQUENCE 239 AA; 27612 MW; B87BD604731BD24 CRC64;

Query Match 41.5%; Score 548; DB 2; Length 239;  
 Best Local Similarity 47.0%; Pred. No. 9.9e-32;

Matches 111; Conservative 44; Mismatches 67; Indels 14; Gaps 6;

QY 30 AADPPPSOLHRS--LYNKLNITLYLEEDDYVHEKNSYQDLSSIDLITVNSC---PY 85  
 DB 2 SDDPMPDHLHSESEPTGCKMKNCKLYDHYVATKRVSKVDFLAHDIYNISDKRKY 61  
 QY 86 DKLTETLNQEMATLFRKQNVDTGYEYVHLYTC--ENAE---SACTYGVYTHN 139  
 DB 62 DKRTLELNDAKRNKDEVDYGSNTVYCTFSKKNQVYGGCKTKHGLGTLNPSKY 121  
 QY 140 ELKEIP--KTIYVYSIDIGSLSPDIEKTKMTYAGELDYKRYKLYTNHQLYTNPSKY 197  
 DB 122 HFDNGNLQNVLYRVEENKRNITISFEVQDCKSVTAQOELDIKARNELINKNLYFENSFV 181  
 QY 198 ETGYIKETIPKNSFWEFFEPF--EFTOSKLYMTIYKDNELTSLNTSOIEVLTTK 231  
 DB 182 ETGYIKETIPKNSFWEFFEPF--EFTOSKLYMTIYKDNELTSLNTSOIEVLTTK 237

## RESULT 14

006535 PRELIMINARY: PRT: 239 AA.  
 ID 006535  
 AC 006535 (TREMBL:01. Created)  
 DT 01-NOV-1996 (TREMBL:01. Last annotation update)  
 DT 01-MAR-2002 (TREMBL:20. Last annotation update)  
 DE Enterotoxin type C-3 (SEC3) (Fragment).  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Staphylococcus.  
 NC NCBI\_FtaxID=1280;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=94011313; PubMed=8406814;  
 RX STRAIN=FRI 909.  
 RT Characterization of novel type C staphylococcal enterotoxins:  
 RT biological and evolutionary implications.  
 RT Infect Immun 61:4254-4262 (1993).  
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
 CC PYOGENIC EXOTOXINS ARE ALL RELATED.

DR PROSITE: P800277: STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE: P800278: STAPH\_STREP\_TOXIN\_2; 1.  
 DR PROSITE: P800279: STAPH\_STREP\_TOXIN\_3; 1.  
 FT NON\_TER  
 SO SEQUENCE 239 AA: 27648 MW: CCCG33046411950 CRC64:

Query Match 41.18; Score 544; DB 2; Length 239;  
 Best Local Similarity 46.28; Pred. No. 1.9e-11;

Matches 109; Conservative 43; Mismatches 70; Indels 14; Gaps 5;

OY 30 ACOOPDPSOLHNS-LYKMLNTYLIESDPTENKYSVDOLSHDLTVNSGP--NY 85  
 DB 2 SOPDPDOLHNSSEFTGNGMKLVDHVSATVSDKFAHDLTVNHKKNNY 61  
 OY 86 DKLATELAKNOEMATLPEKRNVDYGVYHLCYICEN-----AERSACTYGGVTNHEN 139  
 DB 62 DKLATELAKNOEMATLPEKRNVDYGVYHLCYICEN-----AERSACTYGGVTNHEN 139  
 OY 140 HLELP--KTIYKVSIDGISLSDIETENKKNYAOELDKYRKILTDNKKOLYTNGPSK 197  
 DB 122 HDNGMLQNLVLYEENKNTLSEVQTDKSVTAQELDKANFLKNNLTERNSPY 181  
 OY 198 EGTGKIFPKNKESFPEDEPEP--EFTQSKYLMYKONETLDSMTQLEVYLLTK 251  
 DB 182 EGTGKIFPKNKESFPEDEPEP--EFTQSKYLMYKONETLDSMTQLEVYLLTK 237

## RESULT 15

ID 006534 PRELIMINARY: PRT: 239 AA.

AC 006534  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last annotation update)  
 DE Enterotoxin type C (SCOVINE) (fragment).  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;  
 OC Staphylococcus.  
 OX NCBI\_TaxID:1280;  
 RN [1]  
 RS SEQUENCE FROM N.A.  
 RX MEDLINE:94011313; PubMed:8406814;  
 RA Mart J.C., Lyon J.D., Robertson J.R., Luper M., Robach G.A.;  
 RT "Characterization of novel type C staphylococcal enterotoxins:  
 RT biological and evolutionary implications.";  
 RL Infect. Immun. 61:4254-4262(1993).  
 CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
 CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
 CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES  
 CC ENTEROTOXINS ARE ALL RELATED.  
 DR EMBL: L13179; AAA26623.1;  
 DR HSP: P34071; ISR2.  
 DR InterPro: IP801961; Staph/Strep\_toxin.  
 DR Pfam: PF01123; Staph-Strep\_toxin; 1.  
 DR Pfam: PF02876; Staph-Strep\_toxin; 1.  
 DR PRINTS: PR02729; BACTRITOXIN.  
 DR PROSITE: P800277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE: P800278; STAPH\_STREP\_TOXIN\_2; 1.  
 DR PROSITE: P800279; STAPH\_STREP\_TOXIN\_3; 1.  
 FT Enterotoxin; Toxin; Superantigen.  
 FT NON\_TER  
 SO SEQUENCE 239 AA: 27517 MW: F354742619C8D196 CRC64:

Query Match 40.88; Score 539; DB 2; Length 239;  
 Best Local Similarity 45.88; Pred. No. 4.3e-11;

Matches 109; Conservative 46; Mismatches 65; Indels 18; Gaps 6;

OY 30 ACOOPDPSOLHNS-LYKMLNTYLIESDPTENKYSVDOLSHDLTVNSGP--NY 85  
 DB 2 SOPDPDOLHNSSEFTGNGMKLVDHVSATVSDKFAHDLTVNHKKNNY 61  
 OY 86 DKLATELAKNOEMATLPEKRNVDYGVYHLCYICENAGS-----ACTYGGVTNH 137  
 DB 62 DKLATELAKNOEMATLPEKRNVDYGVYHLCYICENAGS-----ACTYGGVTNH 119

OY 138 GHLLELP--KTIYKVSIDGISLSDIETENKKNYAOELDKYRKILTDNKKOLYTNGPS 195  
 DB 120 GHLLELP--KTIYKVSIDGISLSDIETENKKNYAOELDKYRKILTDNKKOLYTNGPS 179  
 OY 196 EGTGKIFPKNKESFPEDEPEP--EFTQSKYLMYKONETLDSMTQLEVYLLTK 251  
 DB 180 EGTGKIFPKNKESFPEDEPEP--EFTQSKYLMYKONETLDSMTQLEVYLLTK 237

Search completed: June 23, 2003, 16:14:55  
 Job time: 40.7024 secs

**THIS PAGE BLANK (USPTO)**



GenCore version: 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: June 23, 2003, 16:10:36 ; Search time 24.0835 seconds  
(without alignments)  
2102.722 Million cell updates/sec

Title: us-10-002-784a-27

Perfect score: 2500

Sequence: 1 MQDDPPDSQLHRSLLVNLQ.....ALGTGGAGGFGNGYSAYVG 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Minimum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2500	100.0	468	9	US-10-002-784A-27
2	1332	53.3	248	9	US-10-002-784A-25
3	1168	46.7	228	9	US-10-002-784A-24
4	1136	45.4	251	1	US-08-882-431-16
5	1136	45.4	251	1	US-08-882-431-16
6	1136	45.4	251	1	US-08-882-431-16
7	1136	45.4	251	1	US-08-882-431-16
8	938.5	37.5	250	9	US-09-870-759-20
9	543	21.7	239	10	US-09-150-947B-12
10	539	21.6	266	9	US-09-870-759-10
11	539	21.6	266	9	US-09-870-759-10
12	532	21.3	266	9	US-10-002-784A-6
13	532	21.3	239	9	US-10-002-784A-10
14	525	21.0	239	9	US-10-002-784A-10
15	523	20.9	266	9	US-10-002-784A-8
16	514	20.6	266	1	US-08-882-431-14
17	514	20.6	266	9	US-10-002-784A-14
18	513	20.5	265	1	US-08-882-431-6
19	509	20.4	266	9	US-09-870-759-12

Sequence 39, Appl  
Sequence 8, Appl  
Sequence 14, Appl  
Sequence 6, Appl  
Sequence 8, Appl  
Sequence 4, Appl  
Sequence 7, Appl  
Sequence 2, Appl  
Sequence 7, Appl  
Sequence 2, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 3, Appl  
Sequence 1, Appl  
Sequence 16, Appl  
Sequence 2, Appl  
Sequence 37, Appl  
Sequence 38, Appl  
Sequence 36, Appl  
Sequence 33, Appl  
Sequence 4, Appl  
Sequence 80, Appl  
Sequence 222, App

20 506.5 20.3 265 1 US-08-882-431-8  
21 397.5 15.9 79 9 US-10-002-784A-39  
22 295.5 11.8 258 9 US-09-870-759-14  
23 281.5 11.3 217 9 US-09-900-766-6  
24 263.5 10.5 257 9 US-09-870-759-8  
25 257.5 10.3 233 9 US-10-002-784A-4  
26 257.5 10.3 233 9 US-10-002-784A-4  
27 257.5 10.3 233 9 US-10-283-838-7  
28 257.5 10.3 233 9 US-10-002-784A-2  
29 256.5 10.3 233 9 US-09-900-766-7  
30 256.5 10.3 233 9 US-10-283-838-8  
31 256 10.2 257 1 US-08-882-431-2  
32 248.2 10.1 233 1 US-08-882-431-4  
33 244.5 9.8 233 9 US-09-900-766-3  
34 244.5 9.8 233 9 US-09-900-766-3  
35 241.5 9.7 672 9 US-09-900-766-1  
36 241 9.6 248 9 US-09-870-759-16  
37 225.5 9.0 233 9 US-09-900-766-2  
38 188 7.5 89 9 US-10-002-784A-37  
39 188 7.5 89 9 US-10-002-784A-36  
40 156 6.2 89 9 US-10-002-784A-36  
41 156 6.2 89 9 US-10-002-784A-36  
42 124.5 5.0 82 9 US-10-002-784A-33  
43 123 4.9 1338 10 US-09-402-100-4  
44 121.5 4.9 789 9 US-10-099-285-80  
45 121 4.8 592 10 US-09-765-272-222

## ALIGNMENTS

RESULT 1  
US-10-002-784A-27  
; Sequence 27, Application US/10002784A  
; Publication No. US20030036644A1  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich, Robert G.  
; TITLE OF INVENTION: Bacterial Superantigen Vaccines  
; FILE REFERENCE: 003/233/SAP  
; CURRENT APPLICATION NUMBER: US/10/002-784A  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776  
; FILING DATE: 97-06-25; 98-09-01  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 27  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: mutant Spea-mutant SpeB fusion  
US-10-002-784A-27

Query Match 100.0%; Score 2500; DB 9; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.2e-185;  
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQDDPPDSQLHRSLLVNLQNYFLYEGDPVTHNKVSDLRSHLDLYNVGSPNWK 60  
Db 1 MQDDPPDSQLHRSLLVNLQNYFLYEGDPVTHNKVSDLRSHLDLYNVGSPNWK 60

QY 61 TELKNOEMATLEKDKNIDYGVYHYHLYCTLCENARSACGGVTNREGNHLTPKKTIVK 120  
Db 61 TELKNOEMATLEKDKNIDYGVYHYHLYCTLCENARSACGGVTNREGNHLTPKKTIVK 120

QY 121 VSDIGLSQSLFDIEFNKNTAQELDYVRYITDNKOLYTNQPSKYETGYIKTFPKNKE 180  
Db 121 VSDIGLSQSLFDIEFNKNTAQELDYVRYITDNKOLYTNQPSKYETGYIKTFPKNKE 180

QY 181 SFNFDFFPEFTQSKYLMYIKDNTLDSNFTQLEVLVTKQPVKSLDSKGHYHNGNP 240  
Db 181 SFNFDFFPEFTQSKYLMYIKDNTLDSNFTQLEVLVTKQPVKSLDSKGHYHNGNP 240

```

QY 241 YNLLPVEIKVPGDSYVQAHATGCATATAQIKYHNTPKGLADYTYTLSSNPYF 300
DB 241 YNLLPVEIKVPGDSYVQAHATGCATATAQIKYHNTPKGLADYTYTLSSNPYF 300
QY 301 NHPKFLAISTROYNNNLPTYSGRSNVQMAISELMADYGVSDMDYGPSSGAGS 360
DB 301 NHPKFLAISTROYNNNLPTYSGRSNVQMAISELMADYGVSDMDYGPSSGAGS 360
QY 361 SRVQALKENYKNSQVQJNNSDFSDQWEAQIDKELSONQPYTQSGKVGCHAFVIGA 420
DB 361 SRVQALKENYKNSQVQJNNSDFSDQWEAQIDKELSONQPYTQSGKVGCHAFVIGA 420
QY 421 DGRNFYHVMNGVSDGFFRLDALNPSALGTGGAGGNGYQSAVWG 468
DB 421 DGRNFYHVMNGVSDGFFRLDALNPSALGTGGAGGNGYQSAVWG 468

```

## RESULT 2

```

US-10-002-784A-25
; Sequence 25, Application US/1002784A
; Publication No. US200300366441
; GENERAL INFORMATION:
; /?3
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO: 25
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-B
US-10-002-784A-25

```

```

Query Match 53.3%; Score 1332; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.5e-95;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 OPVKSLLDSKGIHYNGQNFYNNLLTPVIEKVKPGQSFVQGHAAATGCATATAQIKYHN 280
DB 1 QPVKSLDSKGIHYNGQNFYNNLLTPVIEKVKPGQSFVQGHAAATGCATATAQIKYHN 60
QY 281 YPNKGLADYTYTLSSNPYNNHPKFLAISTROYNNNLPTYSGRSNVQMAISELM 340
DB 61 YPNKGLADYTYTLSSNPYNNHPKFLAISTROYNNNLPTYSGRSNVQMAISELM 120
QY 341 ADVGISVDMYDGPSSGSSSRVQALKENFYNGVHQNRSDFSDQWEAQIDKELSON 400
DB 121 ADVGISVDMYDGPSSGSSSRVQALKENFYNGVHQNRSDFSDQWEAQIDKELSON 180
QY 401 QPVYTGKVGCHAFYIDGADGRNFYHVMNGVSDGFFRLDALNPSALGTGGAGGNG 460
DB 181 QPVYTGKVGCHAFYIDGADGRNFYHVMNGVSDGFFRLDALNPSALGTGGAGGNG 240
QY 461 GYQSAVWG 468
DB 241 GYQSAVWG 248

```

## RESULT 3

```

US-10-002-784A-24
; Sequence 24, Application US/1002784A
; Publication No. US200300366441
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.

```

```

; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO: 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-B
US-10-002-784A-24

Query Match 53.0%; Score 1324.5; DB 9; Length 398;
Best Local Similarity 71.7%; Pred. No. 1.1e-94;
Matches 273; Conservative 20; Mismatches 49; Indels 39; Gaps 10;

QY 95 ERSACI-GGVNREGHLEPKKIVKVSIDGISLQSLFIDEIHNK-KMYTAQELDYKVKY 152
DB 47 QKSAIAKAGARSADIKLD--KYNLGEISGNNMYGYNISTGTVISGDKRSPELIGY 103
QY 153 ITDNQLYVNGPSRYETGYTKIPKAKESFWDFPPPEPTQSKYLIYIKDNELDSNTQ 212
DB 104 STSG-----SFDANKENI-----ASPNES-VYEQIKENKLD--- 136
QY 213 IEVILT---KQPVKSLDSKGIHYNGQNFYNNLLTPVIEKVKPGQSFVQGHAAATGCVA 269
DB 137 --TYAGTAETKOPVVKSLDSKGIHYNGQNFYNNLLTPVIEKVKPGQSFVQGHAAATGCVA 194
QY 270 TATAQIKYHNPKGLADYTYTLSSNPYNNHPKFLAISTROYNNNLPTYSGRS 329
DB 195 TATAQIKYHNPKGLADYTYTLSSNPYNNHPKFLAISTROYNNNLPTYSGRS 254
QY 330 NVQMAISELMADYGVSDMDYGPSSGSSSRVQALKENFYNGVHQNRSDFS-OD 388
DB 255 NVQMAISELMADYGVSDMDYGPSSGSSSRVQALKENFYNGVHQNRSDFS-KQD 314
QY 389 WEAQIDKELSONQPYTQSGKVGCHAFYIDGADGRNFYHVMNGVSDGFFRLDALNP 447
DB 315 WEAQIDKELSONQPYTQSGKVGCHAFYIDGADGRNFYHVMNGVSDGFFRLDALNP 374
QY 448 SALGTGGAGGNGYQSAVWG 468
DB 375 SALGTGGAGGNGYQSAVWG 395

RESULT 4
US-10-002-784A-26
; Sequence 26, Application US/1002784A
; Publication No. US200300366441
; GENERAL INFORMATION:
; /?3
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO: 26
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial sequence
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26

```

Db 1 MODPDSQHRSSLVKKNLONTYELBGPVTHENKVSVDLASHDILTVNSGPNYDKL 60  
 1 MODPDSQHRSSLVKKNLONTYELBGPVTHENKVSVDLASHDILTVNSGPNYDKL 60  
 1 MODPDSQHRSSLVKKNLONTYELBGPVTHENKVSVDLASHDILTVNSGPNYDKL 60  
 61 TELKNQEMATLFKKNKNDIVGEYHYHLYCENMERSACIGGVNREGNHLLEIPKIVK 120  
 61 TELKNQEMATLFKKNKNDIVGEYHYHLYCENMERSACIGGVNREGNHLLEIPKIVK 120  
 121 VSIDGIOSLSFDLETNNKNTYAGELDKYRKYLTDNKLQYTNKSGSYETGYIKFIPKNE 180  
 121 VSIDGIOSLSFDLETNNKNTYAGELDKYRKYLTDNKLQYTNKSGSYETGYIKFIPKNE 180  
 181 SFMPDFPEPFQSKYLMYKKNETLDSNTQIEVYLTK 220  
 181 SFMPDFPEPFQSKYLMYKKNETLDSNTQIEVYLTK 220  
 181 SFMPDFPEPFQSKYLMYKKNETLDSNTQIEVYLTK 220

RESULT 5  
 US-10-002-784-16  
 Sequence 16, Application US/0882431  
 Publication No. US2003009015A1  
 GENERAL INFORMATION:  
 APPLICANT: Robert G. Ulrich,  
 APPLICANT: Robert G. Ulrich,  
 APPLICANT: Robert G. Ulrich,  
 APPLICANT: Robert G. Ulrich,  
 TITLE OF INVENTION: Bacterial Superantigen  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: John Moran  
 CITY: FORT DETRICK  
 STATE: MARYLAND  
 COUNTRY: USA  
 ZIP: 21702-5012  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 7.5  
 SOFTWARE: Microsoft Word 6.0  
 CURRENT APPLICATION DATA: US/08/882, 431  
 FILING DATE: June 25, 1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Moran, John  
 RESIDENCE/DOCKET NUMBER: 26, 313  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 619-2065  
 TELEFAX: (301) 619-7714  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 TYPE: Amino Acid  
 STRANDEDNESS: Unknown  
 TOPOLOGY: Unknown  
 MOLECULE TYPE: Peptide  
 US-08-882-431-16  
 Query Match 45.4%; Score 1136; DB 1; Length 251;  
 Best Local Similarity 98.2%; Pred. No. 2.4e-80;  
 Matches 21; Conservative 1; Mismatches 1; Indels 2; Gaps 2;  
 Db 31 GDDPDSQHRSSLVKKNLONTYELBGPVTHENKVSVDLASHDILTVNSGPNYDKL 90

Oy 62 ELKNQEMATLFKKNKNDIVGEYHYHLYCENMERSACIGGVNREGNHLLEIPKIVK 120  
 Db 91 ELKNQEMATLFKKNKNDIVGEYHYHLYCENMERSACIGGVNREGNHLLEIPKIVK 150  
 Oy 121 VSIDGIOSLSFDLETNNKNTYAGELDKYRKYLTDNKLQYTNKSGSYETGYIKFIPKNE 180  
 Db 151 VSIDGIOSLSFDLETNNKNTYAGELDKYRKYLTDNKLQYTNKSGSYETGYIKFIPKNE 210  
 Oy 181 SFMPDFPEPFQSKYLMYKKNETLDSNTQIEVYLTK 220  
 Db 211 SFMPDFPEPFQSKYLMYKKNETLDSNTQIEVYLTK 251

RESULT 6  
 US-10-002-784-16  
 Sequence 16, Application US/10002784A  
 Publication No. US2003003644A1  
 GENERAL INFORMATION:  
 APPLICANT: Ulrich, Robert G.  
 TITLE OF INVENTION: Bacterial Superantigen Vaccines  
 FILING DATE: 003/23/94  
 CURRENT APPLICATION NUMBER: US/10/002,784A  
 PRIOR FILING DATE: 2001-11-26  
 PRIOR APPLICATION NUMBER: 08/882,431, 09/144,776  
 FILING DATE: 08/05/25; 98-09-01  
 NUMBER OF SEQUENCES: 40  
 SOFTWARE: Apple Macintosh Microsoft Word 6.0  
 SEQ ID NO 16  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE INFORMATION: streptococcal pyrogenic exotoxin-A mutant  
 US-10-002-784A-16  
 Query Match 45.4%; Score 1136; DB 9; Length 251;  
 Best Local Similarity 98.2%; Pred. No. 2.4e-80;  
 Matches 21; Conservative 1; Mismatches 1; Indels 2; Gaps 2;  
 Oy 2 GDDPDSQHRSSLVKKNLONTYELBGPVTHENKVSVDLASHDILTVNSGPNYDKL 61  
 Db 31 GDDPDSQHRSSLVKKNLONTYELBGPVTHENKVSVDLASHDILTVNSGPNYDKL 90  
 Oy 62 ELKNQEMATLFKKNKNDIVGEYHYHLYCENMERSACIGGVNREGNHLLEIPKIVK 120  
 Db 91 ELKNQEMATLFKKNKNDIVGEYHYHLYCENMERSACIGGVNREGNHLLEIPKIVK 150  
 Oy 121 VSIDGIOSLSFDLETNNKNTYAGELDKYRKYLTDNKLQYTNKSGSYETGYIKFIPKNE 180  
 Db 151 VSIDGIOSLSFDLETNNKNTYAGELDKYRKYLTDNKLQYTNKSGSYETGYIKFIPKNE 210  
 Oy 181 SFMPDFPEPFQSKYLMYKKNETLDSNTQIEVYLTK 220  
 Db 211 SFMPDFPEPFQSKYLMYKKNETLDSNTQIEVYLTK 251  
 RESULT 7  
 US-08-973-391A-13  
 Sequence 13, Application US/08973391A  
 Patent No. US20020054887A1  
 GENERAL INFORMATION:  
 APPLICANT: Schlievert, Patricia M.  
 APPLICANT: Rogalski, Manuela  
 APPLICANT: Schlievert, Patricia M.  
 APPLICANT: Schlievert, Patricia M.  
 TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE  
 FILING DATE: 09/03/97  
 CURRENT APPLICATION NUMBER: US/08/973,391A  
 PRIOR FILING DATE: 1998-03-16/0596/10232  
 PRIOR APPLICATION NUMBER: 08/973,391A

PRIOR APPLICATION NUMBER: US 08/480,261  
 PRIOR FILING DATE: 1995-06-07  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 13  
 LENGTH: 251  
 TYPE: PRF  
 ORGANISM: Streptococcus pyogenes  
 US-08-973-351a-13

Query Match  
 Best Local Similarity 44.9%, Score 1122, DB 8; Length 251;  
 Matches 215; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

0Y 1 QODPPSOALHSSLYKVNLTONTYFLGDDPYTHENKVSVDOLSRSHDIYVSGPNTDLTK 61  
 DB 31 QODPPSOALHSSLYKVNLTONTYFLGDDPYTHENKVSVDOLSRSHDIYVSGPNTDLTK 90  
 0Y 62 ELKQNDMAATLEKKNKNDIVGEVYHLYCYLCENMRSCACIYGVYNEHSLIETPKIYVK 130  
 DB 91 ELKQNDMAATLEKKNKNDIVGEVYHLYCYLCENMRSCACIYGVYNEHSLIETPKIYVK 150  
 0Y 121 VSTIGIOSLSPDIETNNKWTAGDLYKAKLIDNKKLITNGSGSTEGYIKFIPKNE 180  
 DB 131 VSTIGIOSLSPDIETNNKWTAGDLYKAKLIDNKKLITNGSGSTEGYIKFIPKNE 210  
 0Y 181 SPMDFEPEPEFPGOSKILMYKONETLDSNT-OIEVYLTTK 220  
 DB 211 SPMDFEPEPEFPGOSKILMYKONETLDSNT-OIEVYLTTK 251

RESULT 8  
 Sequence 8: 870-759-20  
 Patent No. US2002017551A1  
 GENERAL INFORMATION: 5: Mismatches 25; Indels 3; Gaps 3;  
 APPLICANT: TERNAN, David S  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
 CURRENT FILING DATE: 2002-01-14  
 PRIOR APPLICATION NUMBER: US 60/208,128  
 PRIOR FILING DATE: 2000-05-30  
 NUMBER OF SEQ ID NOS: 166  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 166  
 LENGTH: 250  
 TYPE: PRF  
 ORGANISM: Streptococcus pyogenes  
 US-09-870-759-20

Query Match  
 Best Local Similarity 37.5%, Score 938.5; DB 9; Length 250;  
 Matches 185; Conservative 1; Mismatches 25; Indels 3; Gaps 3;

0Y 34 PDSOOLHSSLYKVNLTONTYFLGDDPYTHENKVSVDOLSRSHDIYVSGPNTDLTK 64  
 DB 34 PDSOOLHSSLYKVNLTONTYFLGDDPYTHENKVSVDOLSRSHDIYVSGPNTDLTK 93  
 0Y 65 NQBAATLEKKNKNDIVGEVYHLYCYLCENMRSCACIYGVYNEHSLIETPKIYVK 133  
 DB 94 NQBAATLEKKNKNDIVGEVYHLYCYLCENMRSCACIYGVYNEHSLIETPKIYVK 153  
 0Y 121 VSTIGIOSLSPDIETNNKWTAGDLYKAKLIDNKKLITNGSGSTEGYIKFIPKNE 180  
 DB 131 VSTIGIOSLSPDIETNNKWTAGDLYKAKLIDNKKLITNGSGSTEGYIKFIPKNE 210  
 0Y 181 SPMDFEPEPEFPGOSKILMYKONETLDSNT-OIEVYLTTK 220  
 DB 211 SPMDFEPEPEFPGOSKILMYKONETLDSNT-OIEVYLTTK 250

US-09-150-947b-12  
 Sequence 12, Application US/09150947b  
 Patent No. US2002008211A1  
 GENERAL INFORMATION: 5: Mismatches 67; Indels 18; Gaps 7;  
 APPLICANT: AT&T, Raymond  
 TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS  
 FILE REFERENCE: A31967-PCY-USA-A  
 CURRENT FILING DATE: 1997-12-30  
 PRIOR APPLICATION NUMBER: US/09/150,947b  
 PRIOR FILING DATE: 1997-12-30  
 PRIOR FILING DATE: 1997-12-30  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Patentin version 3.0  
 SEQ ID NO 12  
 LENGTH: 239  
 TYPE: PRF  
 ORGANISM: Staphylococcus aureus  
 US-09-150-947b-12

Query Match  
 Best Local Similarity 44.8%, Score 1144, DB 10; Length 239;  
 Matches 114; Conservative 1; Mismatches 67; Indels 18; Gaps 7;

0Y 2 QODPPSOALHSSLYKVNLTONTYFLGDDPYTHENKVSVDOLSRSHDIYVSGPNTDLTK 61  
 DB 3 QODPPSOALHSSLYKVNLTONTYFLGDDPYTHENKVSVDOLSRSHDIYVSGPNTDLTK 90  
 0Y 58 KKTLEKNDMAATLEKKNKNDIVGEVYHLYCYLCENMRSCACIYGVYNEHSLIETPKIYVK 130  
 DB 63 KKTLEKNDMAATLEKKNKNDIVGEVYHLYCYLCENMRSCACIYGVYNEHSLIETPKIYVK 150  
 0Y 108 QNHETPKIYVNSIDGOSLSPDIETNNKWTAGDLYKAKLIDNKKLITNGSGSTEGYIKFIPKNE 180  
 DB 133 QNHETPKIYVNSIDGOSLSPDIETNNKWTAGDLYKAKLIDNKKLITNGSGSTEGYIKFIPKNE 210  
 0Y 168 EGVYIFIPKNESEFDEPEPEFPGOSKILMYKONETLDSNT-OIEVYLTTK 220  
 DB 183 EGVYIFIPKNESEFDEPEPEFPGOSKILMYKONETLDSNT-OIEVYLTTK 250

RESULT 10  
 Sequence 10: 870-759-10  
 Patent No. US2002017551A1  
 GENERAL INFORMATION: 5: Mismatches 25; Indels 3; Gaps 3;  
 APPLICANT: TERNAN, David S  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE  
 CURRENT FILING DATE: 2002-01-14  
 PRIOR APPLICATION NUMBER: US 60/208,128  
 PRIOR FILING DATE: 2000-05-30  
 NUMBER OF SEQ ID NOS: 166  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 166  
 LENGTH: 250  
 TYPE: PRF  
 ORGANISM: Staphylococcus aureus  
 US-09-870-759-10

Query Match  
 Best Local Similarity 21.6%, Score 541; DB 9; Length 266;  
 Matches 113; Conservative 38; Mismatches 67; Indels 18; Gaps 7;

0Y 2 QODPPSOALHSSLYKVNLTONTYFLGDDPYTHENKVSVDOLSRSHDIYVSGPNTDLTK 61  
 DB 30 QODPPSOALHSSLYKVNLTONTYFLGDDPYTHENKVSVDOLSRSHDIYVSGPNTDLTK 90  
 0Y 58 KKTLEKNDMAATLEKKNKNDIVGEVYHLYCYLCENMRSCACIYGVYNEHSLIETPKIYVK 130  
 DB 63 KKTLEKNDMAATLEKKNKNDIVGEVYHLYCYLCENMRSCACIYGVYNEHSLIETPKIYVK 150

[illegible]

**Tue Jun 24 09:04:14 2003**

us-10-002-784a-27.rapb

Page 6

```

US-08-882-431-10
? Sequence 10, Application US/08882431
? Publication No. US2003005015A1
? GENERAL INFORMATION:
? APPLICANT: G. Ulrich,
? INVENTOR: Mark A. Olson
? APPLICANT: Sina Bavari
? TITLE OF INVENTION: Bacterial Superantigen
? TITLE OF INVENTION: Vaccines
? NUMBER OF SEQUENCES: 16
? CORRESPONDENCE ADDRESS:
? ADDRESS:
? STREET: US Army WMC -504 Scott Street MCMR-JN (John Moran-Patent Atty
? CITY: FORT DETRICK
? STATE: MARYLAND
? COUNTRY: USA
? ZIP: 21702-5012
? COMPUTER READABLE FORM:
? FILED BY THE PATENT COPY 418K
? COMPUTER FILED BY: 418K
? OPERATING SYSTEM: Macintosh 7.5
? SOFTWARE: Microsoft Word 6.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/882,431
? FILING DATE: June 25, 1997
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Moran, John
? REGISTRATION NUMBER: 26,313
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (301) 619-2055
? TELEFAX: (301) 619-7714
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 239
? TYPE: Amino Acid
? STRANDEDNESS: Unknown
? TOPOLOGY: Unknown
? MOLECULE TYPE: Peptide
?
US-08-882-431-10

```

[illegible]

```

RESULT 15
US-10-002-784A-B
: Sequence 8, Application US/10002784A
: Publication No. US2003003664A1
: GENERAL INFORMATION:
: /33
: APPLICANT: Ulrich, Robert G.

```

```

? TITLE OF INVENTION: Bacterial Superantigen Vaccines
?
? FILE REFERENCE: 003/23/5NP
?
? CURRENT APPLICATION NUMBER: US/10/002,784A
?
? PRIOR APPLICATION NUMBER: 2001-11-26
?
? PRIOR FILING DATE: 97-06-25; 98-09-01
?
? INVENTOR: SEO ID NOS: 40
?
? SOURCE: Apple Macintosh Microsoft Word 6.0
?
? SEO ID NO 8
?
? LENGTH: 266
?
? TYPE: PRT
?
? ORGANISM: Artificial sequence
?
? FEATURE:
?
? OTHER INFORMATION: mutant staphylococcal enterotoxin B periplasmic
?
? US-10-002-784A-B

```

[illegible]

Search completed: June 23, 2003, 16:16:39  
Job time : 25.0835 secs

RESULT 15  
US-10-002-784A-B  
Sequence 8, Application US/10002784A-B  
Publication No. US20030036644A1  
GENERAL INFORMATION:  
/33  
APPLICANT: Ulrich, Robert G.



```

DB 234 A1STR0YNNNNLLPYSGHESNOKKAIISLMDVIVISVMDYSGSPSSAGSSRVOYALK 293
OY 369 ENRGYNOGVNIINSDFP--OPENAQUINDELSPNOPIYOC-GRYGHAFYIDGADNRY 426
DB 294 ENRGYNOGVNIINSDFSKQMSQIDIKELSGNOPIYOCVORGNHAFYIDGADNRY 353
OY 427 HVMNGGVSDGDFPDLALNPSALGTGAGGAFPGYQAVYG 468
DB 354 HVMNGGVSDGDFPDLALNPSALGTGAGGAFPGYQAVYG 395

RESULT 2
093102 PRELIMINARY: PRT: 344 AA.
ID 093102: 2001 (Tremblrel. 19, Created)
DB 01-DEC-2001 (Tremblrel. 13, Last annotation update)
DB 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Cysteine protease Spab (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
RN [1] TaxID=1314;
RP SEQUENCE FROM N.A.
RC STRAIN=SP268;
RA Jadon J., Eyal O., Sela S.;
RT Role of carf, hasa, and spab genes in the internalization of
RT Streptococcus pyogenes by epithelial cells.
DB PubMed (PMID 2001) to the EMBL/GenBank/DBJ databases.
DR MEROPS: C10.001; AAA74464.1;
DR InterPro: IP000200; Peptidase_C10.
DR Pfam: PF01640; Peptidase_C10.1.
FT NON-TER 344
FT CHAIN 236
FT SIGNAL 236
FT SEQUENCE 344 AA: 37345 MW: F80A9DE05B41909 CRC64;

Query Match
Best Local Similarity 51.7%; Score 1293.5; DB 2; Length 344;
Matches 231; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

OY 192 FTSKRIYAIKDNELTDSNTQLEVYLT--KQPVVSKSLDSKIHVMGNNYMLATPVI 248
DB 76 FMS-IVYQIKKKKLT-----YAGTKEIKQPVVSKSLDSKIHVMGNNYMLATPVI 129
OY 249 EKVYKGEQSFVGQALATCAVATNQAQIKRHNPKGLADYTTTSSNNRPNRNFPA 308
DB 130 EKVYKGEQSFVGQALATCAVATNQAQIKRHNPKGLADYTTTSSNNRPNRNFPA 189
OY 309 AISTQYNNNNLLPYSGHESNOKKAIISLMDVIVISVMDYSGSPSSAGSSRVOYALK 368
DB 190 AISTQYNNNNLLPYSGHESNOKKAIISLMDVIVISVMDYSGSPSSAGSSRVOYALK 249
OY 369 ENRGYNOGVNIINSDFP--OPENAQUINDELSPNOPIYOC-GRYGHAFYIDGADNRY 426
DB 250 ENRGYNOGVNIINSDFP--OPENAQUINDELSPNOPIYOC-GRYGHAFYIDGADNRY 309
OY 427 HVMNGGVSDGDFPDLALNPSALGTGAGGAFPGYQAVYG 461
DB 310 HVMNGGVSDGDFPDLALNPSALGTGAGGAFPGYQAVYG 344

```

```

GN SPBA
OC Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
RN [1] TaxID=1314;
RP SEQUENCE FROM N.A.
RC STRAIN=SP268;
RA Nelson K., Schlevert P.M., Selander R.K., Musser J.M.;
RT Characterization and clonal distribution of four alleles of the spab
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.
DB Exp. Med. 174:1271-1274(1991).
DB PubMed (PMID 1529) to the EMBL/GenBank/DBJ databases.
DB EMBL: X61570; CAA43770.1;
DB EMBL: X61568; CAA43766.1;
DB EMBL: X61570; CAA43768.1;
DB EMBL: X61571; CAA43769.1;
DB HSP: P08095; 1812;
DR Pfam: PF001961; Sep/Strep_toxin.
DR InterPro: IP001961; Sep/Strep_toxin.
DR Pfam: PF02876; Sep/Strep_toxin.1.
DR PROSITE: PS00277; STAPL_STREP_TOXIN_1.
DR PROSITE: PS00278; STAPL_STREP_TOXIN_2.1.
FT NON-TER <1
FT CHAIN 23
FT SIGNAL 23
FT SEQUENCE 236
FT SIGNAL 236
FT SEQUENCE 236 AA: 27468 MW: 29DFAD575622A84 CRC64;

Query Match
Best Local Similarity 43.9%; Score 1096.5; DB 2; Length 236;
Matches 209; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 2 QQDPSPQSLHSSLYVNIQNIYFYFGDPYTHENYSVYQALRSNOLIVYSGPYTKT 61
DB 23 QQDPSPQSLHSSLYVNIQNIYFYFGDPYTHENYSVYQALRSNOLIVYSGPYTKT 82
OY 62 ELNDEKATLFRKNDIDVEYVYHCTVLENNERSACI-GGVYNRSGNHLTEPKKIYV 120
DB 83 ELNDEKATLFRKNDIDVEYVYHCTVLENNERSACI-GGVYNRSGNHLTEPKKIYV 140
OY 121 VSTDIDIOSLSPDLENNKMYVQGLYVYKRYLTNNKOLYVNSPKXEGYKFKPKKK 180
DB 143 VSTDIDIOSLSPDLENNKMYVQGLYVYKRYLTNNKOLYVNSPKXEGYKFKPKKK 202
OY 181 SFDFEPPRPSTYLYVNDLDSNT 211
DB 203 SFDFEPPRPSTYLYVNDLDSNT 233

RESULT 4
098931 PRELIMINARY: PRT: 422 AA.
ID 098931:
DB 01-MAY-2000 (Tremblrel. 13, Created)
DB 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DB 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Exotoxin A (Fragment).
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
RN [1] TaxID=1314;
RP SEQUENCE FROM N.A.
RC STRAIN=D-05;
RA Bessen D.E., Bessen T.R., Fiorentino T.R., Carlingal R.M.,
RA Hollingshead S.K., Beall B.;

```



RT 'Genetic linkage of exotoxin alleles and emm gene markers for tissue  
 RT 'Interpretation in group A streptococci';  
 DR EMBL: X61557; CA443754.1; -  
 DR HSSP: P08095; 1B12  
 DR InterPro: IP001961; Strep/Strep\_toxin.  
 DR Pfam: PF01123; Strep\_strep\_toxin.1  
 DR PRINTS: PR00279; BACTRTOXIN.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 FT NON\_TER  
 SO SEQUENCE 222 AA; 25759 MW; 488BP/ADCCD91FBA3 CRC64;  
 Query Match 43.8%; Score 1095.5; DB 2; Length 222;  
 Best Local Similarity 98.1%; Pred. No. 4,1e-62;  
 Matches 207; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
 Oy 2 GDDPDSQIHRSSLVKKNLNTLYEGDPVTHENVASVDQLSHDLITVSGFNQDKLT 61  
 Db 11 GDDPDSQIHRSSLVKKNLNTLYEGDPVTHENVASVDQLSHDLITVSGFNQDKLT 70  
 Oy 62 ELKNOEMATLEKDKNIDIGVEYYHLCYLCENASRSACI-GCVTRNGCHLLEPKKIYVA 120  
 Db 71 ELKNOEMATLEKDKNVDIGVEYYHLCYLCENASRSACIYGVTNGHCHLLEPKKIYVA 130  
 Oy 121 VSIDGQSLSFDLETENKKNWVAQEDLYKRYKLTIDNKQDLYTNGPSKYEIGTIFPKNKE 180  
 Db 131 VSIDGQSLSFDLETENKKNWVAQEDLYKRYKLTIDNKQDLYTNGPSKYEIGTIFPKNKE 190  
 Oy 181 SFMDFEPEPEFTOSKIMLYKONETLDSNT 211  
 Db 191 SFMDFEPEPEFTOSKIMLYKONETLDSNT 221  
 RESULT 5  
 ID P97163 PRELIMINARY; PRT: 236 AA.  
 AC P97163; P97164;  
 DT 01-NOV-1996 (TREMBLrel. 03, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DE Type A exotoxin precursor (fragment).  
 GN SPEA.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 CC Streptococcaceae; Streptococcus.  
 NCBI\_TaxID=1314;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-M6AS155; AND NCAS500;  
 RX MEDLINE-92044323; Pubmed-1940804;  
 RA Nelson K., Schlievert P.M., Salander R.K., Musser J.M.;  
 RT 'Characterization and clonal distribution of four alleles of the speA  
 gene encoding pyrogenic exotoxin A (scarlet fever toxin) in  
 Streptococcus pyogenes';  
 RT J. Exp. Med. 174:1271-1274 (1991).  
 DR EMBL: X61556; CA443754.1; -  
 DR EMBL: X61557; CA443755.1; -  
 DR EMBL: X61560; CA443758.1; -  
 DR EMBL: X61555; CA443753.1; -  
 DR EMBL: X61558; CA443756.1; -  
 DR EMBL: X61559; CA443757.1; -  
 DR HSSP: P08095; 1B12  
 DR InterPro: IP001961; Strep/Strep\_toxin.  
 DR Pfam: PF01123; Strep\_strep\_toxin.1  
 DR PRINTS: PR00279; BACTRTOXIN.  
 DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 FT SIGNAL  
 SO SEQUENCE 236 AA; 28784 MW; 287PFLIAB835600 CRC64;

FT NON\_TER 1 1  
 FT SIGNAL <1 22  
 FT CHAIN 23 >236  
 FT NON\_TER 236 236  
 SO SEQUENCE 236 AA; 27844 MW; 3B3PFLIABDC13A84 CRC64;  
 Query Match 43.8%; Score 1095.5; DB 2; Length 236;  
 Best Local Similarity 98.1%; Pred. No. 4,5e-62;  
 Matches 207; Conservative 1; Mismatches 2; Indels 1; Gaps 1;  
 Oy 2 GDDPDSQIHRSSLVKKNLNTLYEGDPVTHENVASVDQLSHDLITVSGFNQDKLT 61  
 Db 23 GDDPDSQIHRSSLVKKNLNTLYEGDPVTHENVASVDQLSHDLITVSGFNQDKLT 82  
 Oy 62 ELKNOEMATLEKDKNIDIGVEYYHLCYLCENASRSACI-GCVTRNGCHLLEPKKIYVA 120  
 Db 83 ELKNOEMATLEKKNVDIGVEYYHLCYLCENASRSACIYGVTNGHCHLLEPKKIYVA 142  
 Oy 121 VSIDGQSLSFDLETENKKNWVAQEDLYKRYKLTIDNKQDLYTNGPSKYEIGTIFPKNKE 180  
 Db 143 VSIDGQSLSFDLETENKKNWVAQEDLYKRYKLTIDNKQDLYTNGPSKYEIGTIFPKNKE 202  
 Oy 181 SFMDFEPEPEFTOSKIMLYKONETLDSNT 211  
 Db 203 SFMDFEPEPEFTOSKIMLYKONETLDSNT 233  
 RESULT 6  
 ID O57453 PRELIMINARY; PRT: 236 AA.  
 AC O57453;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DE Type A exotoxin precursor (fragment).  
 GN SPEA.  
 OS Streptococcus pyogenes.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 CC Streptococcaceae; Streptococcus.  
 NCBI\_TaxID=1314;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-M6AS155; AND NCAS500;  
 RX MEDLINE-92044323; Pubmed-1940804;  
 RA Nelson K., Schlievert P.M., Salander R.K., Musser J.M.;  
 RT 'Characterization and clonal distribution of four alleles of the speA  
 gene encoding pyrogenic exotoxin A (scarlet fever toxin) in  
 Streptococcus pyogenes';  
 RT J. Exp. Med. 174:1271-1274 (1991).  
 DR EMBL: X61562; CA443760.1; -  
 DR EMBL: X61561; CA443759.1; -  
 DR EMBL: X61567; CA443765.1; -  
 DR EMBL: X61564; CA443762.1; -  
 DR EMBL: X61565; CA443763.1; -  
 DR EMBL: X61566; CA443764.1; -  
 DR HSSP: P08095; 1B12  
 DR InterPro: IP001961; Strep/Strep\_toxin.  
 DR Pfam: PF01123; Strep\_strep\_toxin.1  
 DR PRINTS: PR00279; BACTRTOXIN.  
 DR PROSITE: PS00277; STAPH\_STREP\_TOXIN\_1; 1.  
 DR PROSITE: PS00278; STAPH\_STREP\_TOXIN\_2; 1.  
 FT SIGNAL  
 FT NON\_TER 1 1  
 FT SIGNAL <1 22  
 FT CHAIN 23 >236  
 FT NON\_TER 236 236  
 SO SEQUENCE 236 AA; 28784 MW; 287PFLIAB835600 CRC64;  
 Query Match 43.6%; Score 1089.5; DB 2; Length 236;  
 Best Local Similarity 97.6%; Pred. No. 1,1e-61;  
 Matches 206; Conservative 1; Mismatches 3; Indels 1; Gaps 1;



```

RC STRAIN-4951.
RA Kalia A., Bessen D.E.:
RP Presence of streptococcal pyrogenic exotoxin A and C genes in human
RT strains isolated from clinical specimens.
RL Submitted (MAY-2001) to GenBank/Genbank/DBS databases.
DR EMBL: AY049745; AML06066.1; /Genbank/DBS
DR InterPro: IPR001961; Strap/Strep toxin.
DR Pfam: PF01123; Strap_stp_toxin.1.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; UNKNOWN.1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; UNKNOWN.1.
FT NON_TER 222
SQ SEQUENCE 222 AA; 121P846092818P8 CRC64;

Query Match 39.3%; Score 981.5; DB 2; Length 222;
Best Local Similarity 87.7%; Pred. No. 7.1e-55;
Matches 165; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

Oy 2 QODPDPQSOLHRSLSLVKMLONTIFLYEGDPVTHENKASVQOLRSHDLITVNSG--PPVD 57
Db 11 QODPDPQSOLHRSLSLVKMLONTIFLYEGDPVTHENKASVQOLRSHDLITVNSGLDQKAT 70

Oy 62 ELKNOEMATLEFKOKNIDIVGEVYHCLTLENAFESACI--GGTYNRGSGHLEIPKKVYA 120
Db 71 ELKNNKESDLEFNKKNVDIGVGVYVYCYLTKNARACACIGVGVYHSGHLEIPKKVYA 130

Oy 121 VSIDGOSLSFDLETSSKKAVTPOBOLDYVERKHLTDNNQLYTNOPKETEYGIKFSKNOE 180
Db 131 VSIDGOSLSFDLETSSKKAVTPOBOLDYVERKHLTDNNQLYTNOPKETEYGIKFSKNOE 190

Oy 161 SFWDPFPEPFETOSKTYLMTYNDKELTDSNT 211
Db 161 TFWDPFPEPFETOSKTYLMTYNDKELTDSNT 221

RESULT 10
Oy 035678 PRELIMINARY; PRT; 239 AA.
AC 035678 (TribMurel. 01, Created)
DT 01-NOV-1996 (TribMurel. 01, Last sequence update)
DE 01-MAR-2002 (TribMurel. 20, Last annotation update)
DE Enterotoxin (fragments).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
CX NCBI_TaxID=1280.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RL biological and evolutionary implications."
RT Infect. Immun. 61:4254-4262(1993).
DR EMBL: J13376; AAA56620.1; .
DR EMBL: J13376; AAA56620.1; .
DR InterPro: IPR001961; Strap/Strep toxin.
DR Pfam: PF01123; Strap_stp_toxin.1.
DR PRINTS: PR00277; BACTSTREP_TOXIN_1; .
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; .
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; .
SQ SEQUENCE 239 AA; 27618 MW; A13B7B5C6689C2 CRC64;

Query Match 20.6%; Score 516; DB 2; Length 239;
Best Local Similarity 45.1%; Pred. No. 2.7e-25;
Matches 106; Conservative 44; Mismatches 69; Indels 16; Gaps 6;

Oy 2 QODPDPQSOLHRSLSLVKMLONTIFLYEGDPVTHENKASVQOLRSHDLITVNSG--PPVD 57
Db 3 QODPDPQLHRSLSLVKMLONTIFLYEGDPVTHENKASVQOLRSHDLITVNSGLDQKAT 62

```

```

Oy 58 KIKTELKNOEMATLEFKOKNIDIVGEVYHCLTLE-----NAESACIGVGVYHNSGN 110
Db 63 KIKTELKNOEMATLEFKOKNIDIVGEVYHCLTLE-----NAESACIGVGVYHNSGN 122

Oy 111 LSTRK--KIVYKSIDGOSLSFDLETSSKKAVTPOBOLDYVERKHLTDNNQLYTNOPKETE 168
Db 123 FQMKGLQNLIRYENKRNNTISFVGTQSKSTYNOBOLDYVERKHLTDNNQLYTNOPKETE 182

Oy 169 TGYIKFLENNQNTFYDHPADGKFDOSKYLDMYNDKNTVDSKSVIEVHLTTK 237
Db 163 TGYIKFLENNQNTFYDHPADGKFDOSKYLDMYNDKNTVDSKSVIEVHLTTK 237

RESULT 11
Oy 09F0L6 PRELIMINARY; PRT; 271 AA.
AC 09F0L6
DT 01-MAR-2001 (TribMurel. 16, Created)
DT 01-MAR-2002 (TribMurel. 16, Last sequence update)
DT 01-MAR-2002 (TribMurel. 21, Last annotation update)
DE Staphylococcal enterotoxin C-biotype.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
CX NCBI_TaxID=1280.
RX MEDLINE=20566667; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RL Staphylococcus aureus encoding multiple superantigens."
RT J. Bacteriol. 183:6370(2001).
DR EMBL: J40723; AAG29599.1; .
DR EMBL: J40723; AAG29599.1; .
DR InterPro: IPR001961; Strap/Strep toxin.
DR Pfam: PF01123; Strap_stp_toxin.1.
DR PRINTS: PR00279; BACTSTREP_TOXIN_1.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; .
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; .
SQ SEQUENCE 271 AA; 31267 MW; 3493F22B5042F10 CRC64;

Query Match 20.6%; Score 516; DB 2; Length 271;
Best Local Similarity 45.1%; Pred. No. 3.2e-25;
Matches 106; Conservative 44; Mismatches 69; Indels 16; Gaps 6;

Oy 2 QODPDPQSOLHRSLSLVKMLONTIFLYEGDPVTHENKASVQOLRSHDLITVNSG--PPVD 57
Db 35 QODPDPQLHRSLSLVKMLONTIFLYEGDPVTHENKASVQOLRSHDLITVNSGLDQKAT 94

Oy 58 KIKTELKNOEMATLEFKOKNIDIVGEVYHCLTLE-----NAESACIGVGVYHNSGN 110
Db 95 KIKTELKNOEMATLEFKOKNIDIVGEVYHCLTLE-----NAESACIGVGVYHNSGN 154

Oy 111 LSTRK--KIVYKSIDGOSLSFDLETSSKKAVTPOBOLDYVERKHLTDNNQLYTNOPKETE 168
Db 155 FQMKGLQNLIRYENKRNNTISFVGTQSKSTYNOBOLDYVERKHLTDNNQLYTNOPKETE 214

Oy 169 TGYIKFLENNQNTFYDHPADGKFDOSKYLDMYNDKNTVDSKSVIEVHLTTK 237
Db 215 TGYIKFLENNQNTFYDHPADGKFDOSKYLDMYNDKNTVDSKSVIEVHLTTK 269

RESULT 12
Oy 006532 PRELIMINARY; PRT; 239 AA.
AC 006532;
DT 01-NOV-1996 (TribMurel. 01, Created)
DT 01-MAR-2002 (TribMurel. 01, Last sequence update)
DT 01-MAR-2002 (TribMurel. 01, Last annotation update)

```

```

DE Enterotoxin type C-7 (SEC740N) (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OC NCBI_taxid=1285.
RP SEQUENCE FROM N.A.
RX STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RX Murr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT Characterization of novel type C staphylococcal enterotoxins:
RT Infect Immun 61:4254-4262 (1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES
CC PYOGENIC EXOTOXINS ARE ALL RELATED.
EMBL: L13375; AA24619.1; -.
DR Strep/Strep.toxin.
DR InterPro: IPR001961; Strep/Strep.toxin.
DR Pfam: PF01123; Strep.toxin.C.1.
DR PRINTS: PR00279; BACTRITOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN.1.1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN.2.1.
DR Enterotoxin; Toxin; Superantigen.
SQ SEQUENCE 239 AA; 27642 MW; C77009F460CB0645 CRC64;

Query Match 20.6%; Score 515; DB 2; Length 239;
Best Local Similarity 45.1%; Pred. No. 3,le-25;
Matches 106; Conservative 43; Mismatches 70; Indels 16; Gaps 6;

QY 2 QDPDPDPSLRSS-LVKNLNTIYFLYGCPTIENKNSVDOLASRLHTYVNSG---PND 57
DB 3 QDPDPDPLKSSSEFGTDMKNKLYLDHIVSAATKNSVDKRLDLHLITNISDKKLKND 62
ID 006533 PRELIMINARY; PRT; 239 AA.
AC 006533;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1998 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Enterotoxin type C (SEC00PELAN) (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OC NCBI_taxid=1285;
RP SEQUENCE FROM N.A.
RX STRAIN=ANC00PELAN;
RX MEDLINE=94011313; PubMed=8406814;
RX Murr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.
RT Infect Immun 61:4254-4262 (1993).
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: THE DIFFERENT S. AUREUS ENTEROTOXINS AND S. PYOGENES

```

```

CC PYOGENIC EXOTOXINS ARE ALL RELATED.
EMBL: L13378; AA24622.1; -.
DR HSP5; P34071.1; I57E.
DR InterPro: IPR001961; Strep/Strep.toxin.
DR Pfam: PF01123; Strep.toxin.C.1.
DR PRINTS: PR00279; BACTRITOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN.1.1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN.2.1.
DR Enterotoxin; Toxin; Superantigen.
SQ SEQUENCE 239 AA; 27651 MW; A21A95A386AE8625 CRC64;

Query Match 20.6%; Score 515; DB 2; Length 239;
Best Local Similarity 44.7%; Pred. No. 3,le-25;
Matches 105; Conservative 44; Mismatches 70; Indels 16; Gaps 6;

QY 2 QDPDPDPSLRSS-LVKNLNTIYFLYGCPTIENKNSVDOLASRLHTYVNSG---PND 57
DB 3 QDPDPDPLKSSSEFGTDMKNKLYLDHIVSAATKNSVDKRLDLHLITNISDKKLKND 62
ID 005157 PRELIMINARY; PRT; 239 AA.
AC 005157;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last annotation update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OC NCBI_taxid=1285;
RP SEQUENCE FROM N.A.
RX STRAIN=J11;
RX MEDLINE=94011313; PubMed=8406814;
RX Edwards V.M., Deringer J., Rautschke C.V., Bohach G.A.;
RT Characterization of the type C enterotoxin (SEC-canine) produced by
RT Staphylococcus intermedius pyoderma isolates.
RT Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
EMBL: U91546; AA50248.1; -.
DR HSP5; P34313; JCK1. Strep/Strep.toxin.
DR InterPro: IPR001961; Strep/Strep.toxin.
DR Pfam: PF01123; Strep.toxin.C.1.
DR PRINTS: PR00279; BACTRITOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN.1.1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN.2.1.
DR NON-TER
SQ SEQUENCE 239 AA; 27536 MW; D660044660DEA191 CRC64;

Query Match 20.5%; Score 513; DB 2; Length 239;
Best Local Similarity 45.5%; Pred. No. 4,le-25;
Matches 107; Conservative 41; Mismatches 71; Indels 16; Gaps 6;

QY 2 QDPDPDPSLRSS-LVKNLNTIYFLYGCPTIENKNSVDOLASRLHTYVNSG---PND 57
DB 3 QDPDPDPLKSSSEFGTDMKNKLYLDHIVSAATKNSVDKRLDLHLITNISDKKLKND 62

```

**RESULT 15**

DT 01-NOV-1996 (TREMBlere, 01, Created)  
 DT 01-NOV-1996 (TREMBlere, 01, Created)

DE	Enterotoxin type C-4 (SEC4446) (Purified)
DT	01-MAR-2002 ('TREMBlrel. 20, Last annotation update)
DI	01-NOV-1996 ('TREMBlrel. 01, Last sequence update)

05 Staphylococcus aureus.

Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Staphylococcus

NCBI\_TaxID=1280

RP SEQUENCE FROM N.A

RX MEDLINE=94011313:

RT "Characterization of novel type of  
NA marf J.C., Lyon J.D., Roberson J.

biological and evolutionary implications.”;

CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CA

CC -1- SIMILARITY: THE DIFFERENT *S. AUREUS* ENTEROTOXINS AND *S. PYROGENES*

CC PYROGENIC EXOOTOXINS ARE ALL RELATED  
DB EMRI: T1337A: AAA26618 1: -

DR HSSP; P34071; 1SEZ.

DR Pfam; PF01123; Staph\_stp\_toxin; 1.

DR PRINTS; PR00279; BACTRITOXIN.

```

DR PROSITE: PS00278: STAPH STREP TOXIN 3: 1
DR PROSITE: PS00277: STAPH_STREP_TOXIN_1: 1

```

Enterotoxin; Toxin; Superantigen.

SQ SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 20.5%: Score 513: DB 2: Length 239

Best Local Similarity 45.18; Pred. No. 4.1e-25;  
Matches 106: Conservative 43; Mismatches 70. T-4-1- 16 2-2-2- 2

1

[illegible]

02 11 2023 15:00:00

[illegible]

63 KVKTELLNEDLAKKKYKDEVVDYGSNYVNCYFSSKDNVGVKGKTCMYGGITKHGHNH 122

111 LEIP--KIVVKSIDGISOISFDIETNKKMTAQELDVKVRXYLTDNKOQLYTNGPSKYE 168

Db 123 FDNGNLQNLVLRVYENKRNITSEFEVQTDKKS<sup>123</sup>SYTAOELDIKARNFLINKKNLYEENSSPYE 182

169 TCYTKETDPKKESEFWEDEFEED--EETOSKYI MTKKDNEFI DC-AMOTETETETEMK 330

103 MCVTITETUWOWWTHWDGZ DDDYRBS GMAA TTTTUTTTTTT

Search completed: June 23, 2003, 16:14:55

Job time : 70.2976 secs

**THIS PAGE BLANK (USPTO)**



RT Pyrogenes.\*;  
 RN Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).  
 RA Sequence from A.  
 RC STRAIN-MGAS8212. Serotype M18.  
 RA MEDLINE-21927593. PubMed-11917108.  
 RA Smoot J.C., Barblan K.D., Van Gessel J.J., Smoot L.M., Chaussee M.S.,  
 RA Sylva G.L., Sturdevant D.E., Ricklets S.M., Porcella S.F.,  
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,  
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.,  
 RA Genome sequence and comparative microarray analysis of serotype M18  
 RA outbreak *Staphylococcus* strains associated with acute rheumatic fever  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).  
 RN [7]  
 RN PRELIMINARY SEQUENCE OF 28-86 AND 121-398.  
 RA Tomaba K., Elliott S.D., Liu T.-Y.  
 RT Primary structure of zymogen of streptococcal proteinase.\*;  
 RT J. Protein Chem. 11:317-331(1992).  
 RN [8]  
 RN PRELIMINARY SEQUENCE OF 146-398.  
 RA MEDLINE-76190087. PubMed-1270411.  
 RA Tsai J.Y., Kott A.A., Liu T.-Y., Elliott S.D.;  
 RT Primary structure of streptococcal proteinase. III. Isolation of  
 RT cyanogen bromide peptides: complete covalent structure of the  
 RT zymogen.  
 RT J. Biol. Chem. 261:1955-1959(1976).  
 RN [9]  
 RN FUNCTION.  
 RC STRAIN-M2131 / Serotype M49,714;  
 RC MEDLINE-9081733. PubMed-9664206;  
 RA Kao C.-F., Wu J.-J., Tsai P.-J., Kao F.-J., Lei H.-Y., Lin M.T.,  
 RT "Streptococcal pyrogenic exotoxin B induces apoptosis and reduces  
 RT phagocytic activity in U937 cells.\*"  
 RL Infect. Immun. 67:126-130(1999).  
 RN [10]  
 RN FUNCTION.  
 RC STRAIN-A-20 / Serotype M1,71;  
 RC MEDLINE-3936871. PubMed-1035871.  
 RA Tsai P.-J., Lin Y.-S., Kao F.-J., Lei H.-Y., Wu J.-J.;  
 RT "Group A Streptococcus induces apoptosis in human epithelial cells.\*"  
 RL Infect. Immun. 67:4334-4339(1999).  
 CC -1- FUNCTION: IMPORTANT STREPTOCOCCAL VIRULENCE FACTOR WHICH CLEAVES  
 CC HUMAN FIBRONECTIN AND DESMOS VITRONECTIN. ALSO CLEAVES HUMAN  
 CC IL1B PRECURSOR TO FORM BIOLOGICALLY ACTIVE IL1B. CAN INDUCE  
 CC REDUCES PHAGOCYTIC ACTIVITY OF MONOCYTES AND EPITHELIAL CELLS IN VITRO, AND  
 CC ROLE IN BACTERIAL COLONIZATION, INVASION, AND INHIBITION OF WOUND  
 CC HEALING.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage with hydrophobic  
 CC residues at P2, P1 and P1'.  
 CC -1- SUBCELLULAR LOCATION: secreted.  
 CC -1- THE CHAINING FACTOR OF STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE  
 CC FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL DYS-  
 CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF HEMORRAGIC  
 CC FEVER.  
 CC -1- SIMILARITY: BELONGS TO PERTIDASE FAMILY C10.  
 CC THIS MISSED-PROT entry is copyright. It is produced through a collaboration  
 CC between the U.S. Dept. of Health and Human Services and the EMBL collaboration.  
 CC use by non-profit institutions as long as its restrictions on its  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>  
 CC or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).  
 CC EMBL: M65008. AAA26978.1.  
 CC EMBL: M65125. AAA26979.1.  
 CC EMBL: M65126. AAA26982.1.  
 CC EMBL: M65127. AAA26993.1.  
 CC EMBL: L26128. AAA26994.1.  
 CC

DR EMBL: L26130. AAA26996.1.  
 DR EMBL: L26131. AAA26997.1.  
 DR EMBL: L26132. AAA26998.1.  
 DR EMBL: L26133. AAA26999.1.  
 DR EMBL: L26134. AAA27000.1.  
 DR EMBL: L26135. AAA27001.1.  
 DR EMBL: L26136. AAA27002.1.  
 DR EMBL: L26137. AAA27003.1.  
 DR EMBL: L26138. AAA27004.1.  
 DR EMBL: L26139. AAA27005.1.  
 DR EMBL: L26140. AAA27006.1.  
 DR EMBL: L26141. AAA27007.1.  
 DR EMBL: L26142. AAA27008.1.  
 DR EMBL: L26143. AAA27009.1.  
 DR EMBL: L26144. AAA27010.1.  
 DR EMBL: L26145. AAA27011.1.  
 DR EMBL: L26146. AAA27012.1.  
 DR EMBL: L26147. AAA27013.1.  
 DR EMBL: L26148. AAA27014.1.  
 DR EMBL: L26149. AAA27015.1.  
 DR EMBL: L26150. AAA27016.1.  
 DR EMBL: L26151. AAA26981.1.  
 DR EMBL: L26152. AAA26982.1.  
 DR EMBL: L26153. AAA26983.1.  
 DR EMBL: L26154. AAA26984.1.  
 DR EMBL: L26155. AAA26985.1.  
 DR EMBL: L26156. AAA26986.1.  
 DR EMBL: L26157. AAA26987.1.  
 DR EMBL: L26158. AAA26988.1.  
 DR EMBL: L26159. AAA26989.1.  
 DR EMBL: L26160. AAA26990.1.  
 DR EMBL: L26161. AAA26991.1.  
 DR EMBL: L26162. AAA26992.1.  
 DR EMBL: A6104940. AAD17930.1.  
 DR EMBL: A6104948. BAD1672.1.  
 DR EMBL: A6104953. BAD1673.1.  
 DR EMBL: A6104958. BAD1674.1.  
 DR EMBL: A6104963. BAD1675.1.  
 DR EMBL: A6104968. BAD1676.1.  
 DR EMBL: A6104973. BAD1677.1.  
 DR EMBL: A6104978. BAD1678.1.  
 DR EMBL: A6104983. BAD1679.1.  
 DR EMBL: A6104988. BAD1680.1.  
 DR EMBL: A6104993. BAD1681.1.  
 DR EMBL: A6104998. BAD1682.1.  
 DR EMBL: A6105003. BAD1683.1.  
 DR EMBL: A6105008. BAD1684.1.  
 DR EMBL: A6105013. BAD1685.1.  
 DR EMBL: A6105018. BAD1686.1.  
 DR EMBL: A6105023. BAD1687.1.  
 DR EMBL: A6105028. BAD1688.1.  
 DR EMBL: A6105033. BAD1689.1.  
 DR EMBL: A6105038. BAD1690.1.  
 DR EMBL: A6105043. BAD1691.1.  
 DR EMBL: A6105048. BAD1692.1.  
 DR EMBL: A6105053. BAD1693.1.  
 DR EMBL: A6105058. BAD1694.1.  
 DR EMBL: A6105063. BAD1695.1.  
 DR EMBL: A6105068. BAD1696.1.  
 DR EMBL: A6105073. BAD1697.1.  
 DR EMBL: A6105078. BAD1698.1.  
 DR EMBL: A6105083. BAD1699.1.  
 DR EMBL: A6105088. BAD1700.1.  
 DR EMBL: A6105093. BAD1701.1.  
 DR EMBL: A6105098. BAD1702.1.  
 DR EMBL: A6105103. BAD1703.1.  
 DR EMBL: A6105108. BAD1704.1.  
 DR EMBL: A6105113. BAD1705.1.  
 DR EMBL: A6105118. BAD1706.1.  
 DR EMBL: A6105123. BAD1707.1.  
 DR EMBL: A6105128. BAD1708.1.  
 DR EMBL: A6105133. BAD1709.1.  
 DR EMBL: A6105138. BAD1710.1.  
 DR EMBL: A6105143. BAD1711.1.  
 DR EMBL: A6105148. BAD1712.1.  
 DR EMBL: A6105153. BAD1713.1.  
 DR EMBL: A6105158. BAD1714.1.  
 DR EMBL: A6105163. BAD1715.1.  
 DR EMBL: A6105168. BAD1716.1.  
 DR EMBL: A6105173. BAD1717.1.  
 DR EMBL: A6105178. BAD1718.1.  
 DR EMBL: A6105183. BAD1719.1.  
 DR EMBL: A6105188. BAD1720.1.  
 DR EMBL: A6105193. BAD1721.1.  
 DR EMBL: A6105198. BAD1722.1.  
 DR EMBL: A6105203. BAD1723.1.  
 DR EMBL: A6105208. BAD1724.1.  
 DR EMBL: A6105213. BAD1725.1.  
 DR EMBL: A6105218. BAD1726.1.  
 DR EMBL: A6105223. BAD1727.1.  
 DR EMBL: A6105228. BAD1728.1.  
 DR EMBL: A6105233. BAD1729.1.  
 DR EMBL: A6105238. BAD1730.1.  
 DR EMBL: A6105243. BAD1731.1.  
 DR EMBL: A6105248. BAD1732.1.  
 DR EMBL: A6105253. BAD1733.1.  
 DR EMBL: A6105258. BAD1734.1.  
 DR EMBL: A6105263. BAD1735.1.  
 DR EMBL: A6105268. BAD1736.1.  
 DR EMBL: A6105273. BAD1737.1.  
 DR EMBL: A6105278. BAD1738.1.  
 DR EMBL: A6105283. BAD1739.1.  
 DR EMBL: A6105288. BAD1740.1.  
 DR EMBL: A6105293. BAD1741.1.  
 DR EMBL: A6105298. BAD1742.1.  
 DR EMBL: A6105303. BAD1743.1.  
 DR EMBL: A6105308. BAD1744.1.  
 DR EMBL: A6105313. BAD1745.1.  
 DR EMBL: A6105318. BAD1746.1.  
 DR EMBL: A6105323. BAD1747.1.  
 DR EMBL: A6105328. BAD1748.1.  
 DR EMBL: A6105333. BAD1749.1.  
 DR EMBL: A6105338. BAD1750.1.  
 DR EMBL: A6105343. BAD1751.1.  
 DR EMBL: A6105348. BAD1752.1.  
 DR EMBL: A6105353. BAD1753.1.  
 DR EMBL: A6105358. BAD1754.1.  
 DR EMBL: A6105363. BAD1755.1.  
 DR EMBL: A6105368. BAD1756.1.  
 DR EMBL: A6105373. BAD1757.1.  
 DR EMBL: A6105378. BAD1758.1.  
 DR EMBL: A6105383. BAD1759.1.  
 DR EMBL: A6105388. BAD1760.1.  
 DR EMBL: A6105393. BAD1761.1.  
 DR EMBL: A6105398. BAD1762.1.  
 DR EMBL: A6105403. BAD1763.1.  
 DR EMBL: A6105408. BAD1764.1.  
 DR EMBL: A6105413. BAD1765.1.  
 DR EMBL: A6105418. BAD1766.1.  
 DR EMBL: A6105423. BAD1767.1.  
 DR EMBL: A6105428. BAD1768.1.  
 DR EMBL: A6105433. BAD1769.1.  
 DR EMBL: A6105438. BAD1770.1.  
 DR EMBL: A6105443. BAD1771.1.  
 DR EMBL: A6105448. BAD1772.1.  
 DR EMBL: A6105453. BAD1773.1.  
 DR EMBL: A6105458. BAD1774.1.  
 DR EMBL: A6105463. BAD1775.1.  
 DR EMBL: A6105468. BAD1776.1.  
 DR EMBL: A6105473. BAD1777.1.  
 DR EMBL: A6105478. BAD1778.1.  
 DR EMBL: A6105483. BAD1779.1.  
 DR EMBL: A6105488. BAD1780.1.  
 DR EMBL: A6105493. BAD1781.1.  
 DR EMBL: A6105498. BAD1782.1.  
 DR EMBL: A6105503. BAD1783.1.  
 DR EMBL: A6105508. BAD1784.1.  
 DR EMBL: A6105513. BAD1785.1.  
 DR EMBL: A6105518. BAD1786.1.  
 DR EMBL: A6105523. BAD1787.1.  
 DR EMBL: A6105528. BAD1788.1.  
 DR EMBL: A6105533. BAD1789.1.  
 DR EMBL: A6105538. BAD1790.1.  
 DR EMBL: A6105543. BAD1791.1.  
 DR EMBL: A6105548. BAD1792.1.  
 DR EMBL: A6105553. BAD1793.1.  
 DR EMBL: A6105558. BAD1794.1.  
 DR EMBL: A6105563. BAD1795.1.  
 DR EMBL: A6105568. BAD1796.1.  
 DR EMBL: A6105573. BAD1797.1.  
 DR EMBL: A6105578. BAD1798.1.  
 DR EMBL: A6105583. BAD1799.1.  
 DR EMBL: A6105588. BAD1800.1.  
 DR EMBL: A6105593. BAD1801.1.  
 DR EMBL: A6105598. BAD1802.1.  
 DR EMBL: A6105603. BAD1803.1.  
 DR EMBL: A6105608. BAD1804.1.  
 DR EMBL: A6105613. BAD1805.1.  
 DR EMBL: A6105618. BAD1806.1.  
 DR EMBL: A6105623. BAD1807.1.  
 DR EMBL: A6105628. BAD1808.1.  
 DR EMBL: A6105633. BAD1809.1.  
 DR EMBL: A6105638. BAD1810.1.  
 DR EMBL: A6105643. BAD1811.1.  
 DR EMBL: A6105648. BAD1812.1.  
 DR EMBL: A6105653. BAD1813.1.  
 DR EMBL: A6105658. BAD1814.1.  
 DR EMBL: A6105663. BAD1815.1.  
 DR EMBL: A6105668. BAD1816.1.  
 DR EMBL: A6105673. BAD1817.1.  
 DR EMBL: A6105678. BAD1818.1.  
 DR EMBL: A6105683. BAD1819.1.  
 DR EMBL: A6105688. BAD1820.1.  
 DR EMBL: A6105693. BAD1821.1.  
 DR EMBL: A6105698. BAD1822.1.  
 DR EMBL: A6105703. BAD1823.1.  
 DR EMBL: A6105708. BAD1824.1.  
 DR EMBL: A6105713. BAD1825.1.  
 DR EMBL: A6105718. BAD1826.1.  
 DR EMBL: A6105723. BAD1827.1.  
 DR EMBL: A6105728. BAD1828.1.  
 DR EMBL: A6105733. BAD1829.1.  
 DR EMBL: A6105738. BAD1830.1.  
 DR EMBL: A6105743. BAD1831.1.  
 DR EMBL: A6105748. BAD1832.1.  
 DR EMBL: A6105753. BAD1833.1.  
 DR EMBL: A6105758. BAD1834.1.  
 DR EMBL: A6105763. BAD1835.1.  
 DR EMBL: A6105768. BAD1836.1.  
 DR EMBL: A6105773. BAD1837.1.  
 DR EMBL: A6105778. BAD1838.1.  
 DR EMBL: A6105783. BAD1839.1.  
 DR EMBL: A6105788. BAD1840.1.  
 DR EMBL: A6105793. BAD1841.1.  
 DR EMBL: A6105798. BAD1842.1.  
 DR EMBL: A6105803. BAD1843.1.  
 DR EMBL: A6105808. BAD1844.1.  
 DR EMBL: A6105813. BAD1845.1.  
 DR EMBL: A6105818. BAD1846.1.  
 DR EMBL: A6105823. BAD1847.1.  
 DR EMBL: A6105828. BAD1848.1.  
 DR EMBL: A6105833. BAD1849.1.  
 DR EMBL: A6105838. BAD1850.1.  
 DR EMBL: A6105843. BAD1851.1.  
 DR EMBL: A6105848. BAD1852.1.  
 DR EMBL: A6105853. BAD1853.1.  
 DR EMBL: A6105858. BAD1854.1.  
 DR EMBL: A6105863. BAD1855.1.  
 DR EMBL: A6105868. BAD1856.1.  
 DR EMBL: A6105873. BAD1857.1.  
 DR EMBL: A6105878. BAD1858.1.  
 DR EMBL: A6105883. BAD1859.1.  
 DR EMBL: A6105888. BAD1860.1.  
 DR EMBL: A6105893. BAD1861.1.  
 DR EMBL: A6105898. BAD1862.1.  
 DR EMBL: A6105903. BAD1863.1.  
 DR EMBL: A6105908. BAD1864.1.  
 DR EMBL: A6105913. BAD1865.1.  
 DR EMBL: A6105918. BAD1866.1.  
 DR EMBL: A6105923. BAD1867.1.  
 DR EMBL: A6105928. BAD1868.1.  
 DR EMBL: A6105933. BAD1869.1.  
 DR EMBL: A6105938. BAD1870.1.  
 DR EMBL: A6105943. BAD1871.1.  
 DR EMBL: A6105948. BAD1872.1.  
 DR EMBL: A6105953. BAD1873.1.  
 DR EMBL: A6105958. BAD1874.1.  
 DR EMBL: A6105963. BAD1875.1.  
 DR EMBL: A6105968. BAD1876.1.  
 DR EMBL: A6105973. BAD1877.1.  
 DR EMBL: A6105978. BAD1878.1.  
 DR EMBL: A6105983. BAD1879.1.  
 DR EMBL: A6105988. BAD1880.1.  
 DR EMBL: A6105993. BAD1881.1.  
 DR EMBL: A6105998. BAD1882.1.  
 DR EMBL: A6106003. BAD1883.1.  
 DR EMBL: A6106008. BAD1884.1.  
 DR EMBL: A6106013. BAD1885.1.  
 DR EMBL: A6106018. BAD1886.1.  
 DR EMBL: A6106023. BAD1887.1.  
 DR EMBL: A6106028. BAD1888.1.  
 DR EMBL: A6106033. BAD1889.1.  
 DR EMBL: A6106038. BAD1890.1.  
 DR EMBL: A6106043. BAD1891.1.  
 DR EMBL: A6106048. BAD1892.1.  
 DR EMBL: A6106053. BAD1893.1.  
 DR EMBL: A6106058. BAD1894.1.  
 DR EMBL: A6106063. BAD1895.1.  
 DR EMBL: A6106068. BAD1896.1.  
 DR EMBL: A6106073. BAD1897.1.  
 DR EMBL: A6106078. BAD1898.1.  
 DR EMBL: A6106083. BAD1899.1.  
 DR EMBL: A6106088. BAD1900.1.  
 DR EMBL: A6106093. BAD1901.1.  
 DR EMBL: A6106098. BAD1902.1.  
 DR EMBL: A6106103. BAD1903.1.  
 DR EMBL: A6106108. BAD1904.1.  
 DR EMBL: A6106113. BAD1905.1.  
 DR EMBL: A6106118. BAD1906.1.  
 DR EMBL: A6106123. BAD1907.1.  
 DR EMBL: A6106128. BAD1908.1.  
 DR EMBL: A6106133. BAD1909.1.  
 DR EMBL: A6106138. BAD1910.1.  
 DR EMBL: A6106143. BAD1911.1.  
 DR EMBL: A6106148. BAD1912.1.  
 DR EMBL: A6106153. BAD1913.1.  
 DR EMBL: A6106158. BAD1914.1.  
 DR EMBL: A6106163. BAD1915.1.  
 DR EMBL: A6106168. BAD1916.1.  
 DR EMBL: A6106173. BAD1917.1.  
 DR EMBL: A6106178. BAD1918.1.  
 DR EMBL: A6106183. BAD1919.1.  
 DR EMBL: A6106188. BAD1920.1.  
 DR EMBL: A6106193. BAD1921.1.  
 DR EMBL: A6106198. BAD1922.1.  
 DR EMBL: A6106203. BAD1923.1.  
 DR EMBL: A6106208. BAD1924.1.  
 DR EMBL: A6106213. BAD1925.1.  
 DR EMBL: A6106218. BAD1926.1.  
 DR EMBL: A6106223. BAD1927.1.  
 DR EMBL: A6106228. BAD1928.1.  
 DR EMBL: A6106233. BAD1929.1.  
 DR EMBL: A6106238. BAD1930.1.  
 DR EMBL: A6106243. BAD1931.1.  
 DR EMBL: A6106248. BAD1932.1.  
 DR EMBL: A6106253. BAD1933.1.  
 DR EMBL: A6106258. BAD1934.1.  
 DR EMBL: A6106263. BAD1935.1.  
 DR EMBL: A6106268. BAD1936.1.  
 DR EMBL: A6106273. BAD1937.1.  
 DR EMBL: A6106278. BAD1938.1.  
 DR EMBL: A6106283. BAD1939.1.  
 DR EMBL: A6106288. BAD1940.1.  
 DR EMBL: A6106293. BAD1941.1.  
 DR EMBL: A6106298. BAD1942.1.  
 DR EMBL: A6106303. BAD1943.1.  
 DR EMBL: A6106308. BAD1944.1.  
 DR EMBL: A6106313. BAD1945.1.  
 DR EMBL: A6106318. BAD1946.1.  
 DR EMBL: A6106323. BAD1947.1.  
 DR EMBL: A6106328. BAD1948.1.  
 DR EMBL: A6106333. BAD1949.1.  
 DR EMBL: A6106338. BAD1950.1.  
 DR EMBL: A6106343. BAD1951.1.  
 DR EMBL: A6106348. BAD1952.1.  
 DR EMBL: A6106353. BAD1953.1.  
 DR EMBL: A6106358. BAD1954.1.  
 DR EMBL: A6106363. BAD1955.1.  
 DR EMBL: A6106368. BAD1956.1.  
 DR EMBL: A6106373. BAD1957.1.  
 DR EMBL: A6106378. BAD1958.1.  
 DR EMBL: A6106383. BAD1959.1.  
 DR EMBL: A6106388. BAD1960.1.  
 DR EMBL: A6106393. BAD1961.1.  
 DR EMBL: A6106398. BAD1962.1.  
 DR EMBL: A6106403. BAD1963.1.  
 DR EMBL: A6106408. BAD1964.1.  
 DR EMBL: A6106413. BAD1965.1.  
 DR EMBL: A6106418. BAD1966.1.  
 DR EMBL: A6106423. BAD1967.1.  
 DR EMBL: A6106428. BAD1968.1.  
 DR EMBL: A6106433. BAD1969.1.  
 DR EMBL: A6106438. BAD1970.1.  
 DR EMBL: A6106443. BAD1971.1.  
 DR EMBL: A6106448. BAD1972.1.  
 DR EMBL: A6106453. BAD1973.1.  
 DR EMBL: A6106458. BAD1974.1.  
 DR EMBL: A6106463. BAD1975.1.  
 DR EMBL: A6106468. BAD1976.1.  
 DR EMBL: A6106473. BAD1977.1.  
 DR EMBL: A6106478. BAD1978.1.  
 DR EMBL: A6106483. BAD1979.1.  
 DR EMBL: A6106488. BAD1980.1.  
 DR EMBL: A6106493. BAD1981.1.  
 DR EMBL: A6106498. BAD1982.1.  
 DR EMBL: A6106503. BAD1983.1.  
 DR EMBL: A6106508. BAD1984.1.  
 DR EMBL: A6106513. BAD1985.1.  
 DR EMBL: A6106518. BAD1986.1.  
 DR EMBL: A6106523. BAD1987.1.  
 DR EMBL: A6106528. BAD1988.1.  
 DR EMBL: A6106533. BAD1989.1.  
 DR EMBL: A6106538. BAD1990.1.  
 DR EMBL: A6106543. BAD1991.1.  
 DR EMBL: A6106548. BAD1992.1.  
 DR EMBL: A6106553. BAD1993.1.  
 DR EMBL: A6106558. BAD1994.1.  
 DR EMBL: A6106563. BAD1995.1.  
 DR EMBL: A6106568. BAD1996.1.  
 DR EMBL: A6106573. BAD1997.1.  
 DR EMBL: A6106578. BAD1998.1.  
 DR EMBL: A6106583. BAD1999.1.  
 DR EMBL: A6106588. BAD2000.1.  
 DR EMBL: A6106593. BAD2001.1.  
 DR EMBL: A6106598. BAD2002.1.  
 DR EMBL: A6106603. BAD2003.1.  
 DR EMBL: A6106608. BAD2004.1.  
 DR EMBL: A6106613. BAD2005.1.  
 DR EMBL: A6106618. BAD2006.1.  
 DR EMBL: A6106623. BAD2007.1.  
 DR EMBL: A6106628. BAD2008.1.  
 DR EMBL: A6106633. BAD2009.1.  
 DR EMBL: A6106638. BAD2010.1.  
 DR EMBL: A6106643. BAD2011.1.  
 DR EMBL: A6106648. BAD2012.1.  
 DR EMBL: A6106653. BAD2013.1.  
 DR EMBL: A6106658. BAD2014.1.  
 DR EMBL: A6106663. BAD2015.1.  
 DR EMBL: A6106668. BAD2016.1.  
 DR EMBL: A6106673. BAD2017.1.  
 DR EMBL: A6106678. BAD2018.1.  
 DR EMBL: A6106683. BAD2019.1.  
 DR EMBL: A6106688. BAD2020.1.  
 DR EMBL: A6106693. BAD2021.1.  
 DR EMBL: A6106698. BAD2022.1.  
 DR EMBL: A6106703. BAD2023.1.  
 DR EMBL: A6106708. BAD2024.1.  
 DR EMBL: A6106713. BAD2025.1.  
 DR EMBL: A6106718. BAD2026.1.  
 DR EMBL: A6106723. BAD2027.1.  
 DR EMBL: A6106728. BAD2028.1.  
 DR EMBL: A6106733. BAD2029.1.  
 DR EMBL: A6106738. BAD2030.1.  
 DR EMBL: A6106743. BAD2031.1.  
 DR EMBL: A6106748. BAD2032.1.  
 DR EMBL: A6106753. BAD2033.1.  
 DR EMBL: A6106758. BAD2034.1.  
 DR EMBL: A6106763. BAD2035.1.  
 DR EMBL: A6106768. BAD2036.1.  
 DR EMBL: A6106773. BAD2037.1.  
 DR EMBL: A6106778. BAD2038.1.  
 DR EMBL: A6106783. BAD2039.1.  
 DR EMBL: A6106788. BAD2040.1.  
 DR EMBL: A6106793. BAD2041.1.  
 DR EMBL: A6106798. BAD2042.1.  
 DR EMBL: A6106803. BAD2043.1.  
 DR EMBL: A6106808. BAD2044.1.  
 DR EMBL: A6106813. BAD2045.1.  
 DR EMBL: A6106818. BAD2046.1.  
 DR EMBL: A6106823. BAD2047.1.  
 DR EMBL: A6106828. BAD2048.1.  
 DR EMBL: A6106833. BAD2049.1.  
 DR EMBL: A6106838. BAD2050.1.



	Query	Subject	Score	137.5	DB 1	Length	398
			51.1%				
			Best Local Similarity	91.5%		Pred.	No. 3.9e-40
			Matches	258	Conservative	5	Mismatches
						8	Indels
						11	Gaps
Qy	197	FTOSKTKLMIYKIDTSLDSTLSDTLEVLYLT...KQPVVKSILDSKDHVYKQGNENPILNLPVT	248				
Db	120	PHSS...VDSQVQKATCTP...TTACTMETKIDQPVVKSILDSKDHVYKQGNENPILNLPVT	173				
Qy	249	EKKYGGVDSQVQKATCTP...VATVATQIMKNTNPKKGLADTYYTSSNNPYNPKHKLPA	308				
Db	174	EKKYGGVDSQVQKATCTP...VATVATQIMKNTNPKKGLADTYYTSSNNPYNPKHKLPA	233				
Qy	309	AISTRQVNNKNTLFTYSGRSNYSNOKMAISELMDADVGIISVDMDYGFSSGSSGRVORALK	368				
Db	234	AISTRQVNNKNTLFTYSGRSNYSNOKMAISELMDADVGIISVDMDYGFSSGSSGRVORALK	293				
Qy	359	ENCTYNSVHAIQNSQSP...QDMQDIDKTSQNDQPYVQSG...QKYGGAHAPYQAGDNPNY	456				
Db	294	ENCTYNSVHAIQNSQSP...QDMQDIDKTSQNDQPYVQSG...QKYGGAHAPYQAGDNPNY	353				
Qy	427	HYVNGAGVSDGFRTDLALNPSALATGGGAGFNQVGYSAVNG	468				
Db	354	HYVNGAGVSDGFRTDLALNPSALATGGGAGFNQVGYSAVNG	395				
RESULT 2							
IC	SPEA_STRPY	STANDARD	PRG	251	AA		
ID	P08095						
DT	01-AUG-1988 (rel. 08)	Created					
DT	01-JUN-1990 (rel. 13)	Last sequence update					
DT	15-JUN-2002 (rel. 41)	Last annotation update					
DE	Streptococcus type A precursor (Scarlet fever toxin) (Erythrogenic toxin) (SPE A)						
DE	SPEA OR SPEYA.0399.						
OS	Streptococcus pyogenes, and						
OS	Streptococcus pyogenes (serotype M18).						
OC	Bacteria: Firmicutes: Lactobacillales; Streptococcaceae; Streptococcus.						
OX	NCBI_TaxID=1314, 186103;						
RL	SEQUENCE FROM N.A.						
RL	MEDLINE=86166804; PubMed=3514452;						
RL	Weeks C.R., Ferretti J.J.:						
RT	"Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage 112.";						
RT	Infect. Immun. 57:144-150(1986).						
RL	SEQUENCE FROM N.A.						
RL	MEDLINE=2193753; PubMed=11917108.						
RL	Smoot J.C., Barbhan K.D., Van Gmel J.J., Smoot L.M., Chaussee M.S.,						
RA	Sylvia G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,						
RA	Parfitt L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,						
RA	Kapur V., Daly J.A., Vasey L.G., Musser J.M.:						
RA	Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever						
RA	Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).						
RA	X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).						
RA	MEDLINE=9094887; PubMed=9878045;						
RA	Papageorgiou A.C., Collins C.M., Kuran D.M., Kline J.B.,						
RA	O'Brien S.M., Tranker H.S., Acharya K.R.:						

```

RT      *Structural basis for the recognition of superantigen streptococcal
RT      pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RL      receptors."
RL      PMID J. 18-9-21(1999).
Cc       -1- SUBUNIT: Binds to major histocompatibility complex class II beta
Cc       chain.
Cc       -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
Cc       THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
Cc       FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
Cc       DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATOID
Cc       FEVER.
Cc       -1- SIMILARITY: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
Cc       -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
Cc       FAMILY.
Cc       -----
Cc       This SWISS-PROT entry is copyright. It is produced through a collaboration
Cc       between the Swiss Institute of Bioinformatics and the EMBL outstation -
Cc       the European Bioinformatics Institute. There are no restrictions on its
Cc       use by non-profit institutions as long as its content is in no way
Cc       modified and this statement is not removed. Usage by and for commercial
Cc       entities requires a license agreement (see http://www.isb-jlb.chv.unimuench.de)
Cc       or contact the EBI.
Cc       CC
Cc       EMBL; U040453; AAC48688.1; ?
Cc       DR     EMBL; X03929; CA27568.1; ?
Cc       DR     EMBL; AE009892; ALN9741.1; ?
Cc       DR     PIR; A26152; A26152.
Cc       DR     PIR; Z26959; S26959.
Cc       DR     UNIPROT; IPI001961; Strep/Strep.toxin.
Cc       DR     InterPro: IP001961;
Cc       DR     Pfam: PF02876; Strep_Strep_toxin; 1.
Cc       DR     Pfam: PF02876; Strep_Strep_toxin.C; 1.
Cc       DR     PRINTS; PR00279; BACTRILTOXIN.
Cc       DR     PROSITE; PS00227; STAPH_STREP_TOXIN_1; 1.
Cc       DR     PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
Cc       KM
Cc       toxin; Signal; 30-strucure.
Cc       FT
Cc       FT CHAIN          1   251
Cc       FT DISULFID      117 128
Cc       FT CONFLICT      6    6
Cc       FT CONFLICT     17   18
Cc       FT CONFLICT     25   35
Cc       FT CONFLICT     40   40
Cc       FT CONFLICT     43   43
Cc       FT CONFLICT     47   59
Cc       FT CONFLICT     129 139
Cc       FT CONFLICT     165 178
Cc       FT CONFLICT
Cc       FT CONFLICT
Cc       SQ SEQUENCE      251 AA; 29246 MW; 54001FF4ACCBFC03 CIRCSPEC;
Cc
Cc Query Match      45.2%; Score 1139 DB 1; Length 251;
Cc      Identity 97.7%;
Cc      Matches 216; Conservative 1; Mismatches 2; Indels 2; Gaps 2;
Cc
Cc      1 OGDPPDSGLNRSLSYLVKLNQNIYLYLEDDPYVHNKKYSVDLSISDIITVNSGPNYDLKT 61
Cc      2 OGDPPDSGLNRSLSYLVKLNQNIYLYLEDDPYVHNKKYSVDLSISDIITVNSGPNYDLKT 61
Cc      3 QODPDPSGLNRSLSYLVKLNQNIYLYLEDDPYVHNKKYSVDLSISDIITVNSGPNYDLKT 90
Cc      62 ELKNQPMALPFKDNNDIVIGVEHYLLCYLCENAESAGICT-GGMNREGONILLERIKTYK 120
Cc      91 ELKNQPMALPFKDNNDIVIGVEHYLLCYLCENAESAGICT-GGMNREGONILLERIKTYK 150
Cc
Cc      121 VSADJGSGLSPDIEFNKKWKAQAELDYKFKRYLTLDNQKLYTNMGSGYSTGYTKRFPKPNNK 180
Cc      151 VSADJGSGLSPDIEFNKKWKAQAELDYKFKRYLTLDNQKLYTNMGSGYSTGYTKRFPKPNNK 210
Cc      181 SNRPDPPEPRPGEPSTOSKYMTYKUNEDSNST--OIVETLYTK 220
Cc      211 SNRPDPPEPRPGEPSTOSKYMTYKUNEDSNSTSOILEVYLTK 251

```

[illegible]



[illegible]



RP SEQUENCE FROM N.A.  
RX STRAIN-9MW:  
RX MEDLINE=22040717; PubMed=13043478;  
RA Hoshino T., Takahashi F., Kikuchi M., Yuzawa H., Aoki K.-I., Ogunchi A.,  
RA Yamamoto K., Nomura N., Asano K., Nakai T., Kuroda H., Cui L.,  
RA Yamamoto K., Hiratsuyu K.:  
RT "Genome and virulence determinants of high virulence community-  
RT acquired MRSA." :  
RL Lancet 359:1819-1827(2002).  
RL  
RL (2)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80686932; PubMed=33354833;  
RA Beller M.J., Mekalanos J.J.:  
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene."  
RL J. Bacteriol. 170:34-41(1988).  
RL (3)  
RP SEQUENCE OF 25-257  
RX MEDLINE=87222833; PubMed=3841105;  
RA Huang W., Wang X., Wu Z., Bergdoll M.S., Schantz E.J.:  
RT "The amino acid sequence of staphylococcal enterotoxin A." :  
RL J. Biol. Chem. 263:7006-7033(1987).  
RL (4)  
RX MEDLINE=95356488; PubMed=7628431;  
RA Schmid E.M., Zaitsev I., Zaitsev S., Dohlsien M., Kolland T.,  
RA Schilleberg P.N., Olsen I., Stenstrom L.A.,  
RT "Crystal structure of the superantigen staphylococcal enterotoxin  
RT type A." :  
RL EMBO J. 14:3292-3301(1995).  
RN (5)  
RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).  
RX MEDLINE=97113057; PubMed=8643378;  
RA Sundstedt M., Hallén B., Svensson A., Schmid E., Dohlsien M.,  
RA Sundstedt M., Hallén B., Svensson A., Schmid E., Dohlsien M.,  
RT "The Co-crystal structure of staphylococcal enterotoxin type A with  
RT Zn2+ at 2.7 Å resolution. Implications for major histocompatibility  
RT complex class II binding." :  
RL J. Biol. Chem. 271:32212-32216(1996).  
RN (6)  
RX 3D-STRUCTURE MODELING.  
RX MEDLINE=96022987; PubMed=7552730;  
RA Samaninani S., Frey W.F. Jr., Fletcher J., Sax M.:  
RT "Residues defining V beta specificity in staphylococcal  
RT enterotoxins." :  
RL Nat. Struct. Biol. 2:680-686(1995).  
RN (7)  
RX COMPARISON OF STRUCTURE OF SEA AND SEB2.  
RX MEDLINE=97353233; PubMed=9101070;  
RA Smith M.E., Swanson A.C., Swanson L.A., Acharya K.R.:  
RT "A structural and functional comparison of staphylococcal  
RT enterotoxins A and C2 reveals remarkable similarity and  
RT dissimilarity." :  
RL J. Mol. Biol. 269:270-280(1997).  
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary  
CC for the toxin interaction with MHC Class II.  
CC -1- SUBCELLULAR LOCATION: secreted.  
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION  
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.  
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.  
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN  
CC FAMILY.  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the Swiss Biotechnology Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announcements>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL AB004628 BK095754.1;







KR	PROSITE:PS00278; STAPH_STEEP_TOXIN_N2.1.	
DR	KW Toxin:Signal; Complete proteome.	
FT	SIGNAL	1 24
ET	CHAIN	25 234
NO	SEQUENCE	234 AA; 217662 MW; 49525C949A8A2052 CRC64;
50	QUERY MATCH	
Best Local Similarity	21.38%	Score 157; DR 3; Length 234;
Matches	48: Conservative 40; Mismatches 80; Indels 50; Gaps 8;	
QY	34 ENKASVDLSDHIDIVSPGPNVTK-----LATELKNQDMA-----	69
DB	26 ENIK--DKIKSRPAANTKCTDEWEIAFVTTNSIIHTKQKSCILYVDSISLGIT	83
QY	70 -LEKDKNIDIVGCHYHILCYLCEN-----AKRSACIGATVREGNCHILETPKRI	117
DB	84 DQELIGKQDVDFGLPNSPPYVDNIIGSTYKHSQGNSTLQPVGLNLDGKQEVYLPSELA	143

[illegible]



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2003, 16:10:06 ; Search time 34.4979 seconds

(Without alignments)  
1304.163 Million cell updates/sec

Title: US-10-002-784a-27

Perfect score: 2500

Sequence: 1 XQDDPDSQHRSSLVKMLD.....ALGTGGAGGNGGSAVNG 468

Scoring table:

BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR.73.\*  
2: PIR1.\*  
3: PIR2.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1327.5	53.1	398	2 A37768	streptococcal pyro
2	1198	47.9	398	2 BP50P	streptococcal (EC 3
3	1129	43.2	231	1 S29659	exotoxin type A pr
4	1084.5	43.6	231	1 S1783	exotoxin type A pr
5	1089.5	43.6	236	2 S1783	exotoxin type A pr
6	986.5	39.5	236	2 S1789	streptococcal pyro
7	938.5	37.5	250	1 A26152	streptococcal pyro
8	541	20.6	266	1 ENSAB6	enterotoxin B pr
9	513	20.5	266	2 S11885	enterotoxin C3 - S
10	510	20.4	266	2 A60114	enterotoxin C-1 pr
11	492	20.4	266	1 ENSAB6	enterotoxin C-1 pr
12	444	17.6	886	2 T10890	enterococcal prote
13	422	16.9	886	2 T10890	enterococcal prote
14	303.5	12.1	136	2 A89969	enterotoxin D pr
15	295.5	11.8	280	2 A33953	enterotoxin D pr
16	291.5	11.2	260	2 E89969	enterotoxin D pr
17	279.5	11.2	260	2 C89969	enterotoxin D pr
18	267.5	10.5	250	2 G89969	enterotoxin D pr
19	262.5	10.5	250	2 G89969	enterotoxin D pr
20	257.5	10.3	257	2 A28664	enterotoxin D pr
21	256.5	10.3	257	2 A28179	enterotoxin D pr
22	237.5	9.5	239	2 D89969	enterotoxin D pr
23	218	8.7	242	2 C89969	enterotoxin D pr
24	193	7.3	235	2 A30509	exotoxin C precurs
25	183	6.5	235	2 B89969	exotoxin C precurs
26	154.7	6.3	235	2 C89969	hypothetical prote
27	137	5.5	2500	2 C71865	hypothetical prote
28	133.5	5.3	231	2 D89807	hypothetical prote
29	124.5	5.0	750	2 G81361	probable flagellin

## ALIGNMENTS

RESULT 1	30	124.5	5.0	1183	2 F90559	conserved hypothet
A37768	31	123.5	4.9	616	2 G82885	hypothetical prote
streptococcal pyrogenic exotoxin type B precursor - Streptococcus pyogenes	32	123	4.9	227	2 C89808	exotoxin B1 (limpor
C:Species: Streptococcus pyogenes	33	123	4.9	1215	2 B48281	cytochrome-c-associat
C:Date: 31-May-1991 #sequence-revision 31-May-1991 #text-change 22-Jun-1999	34	122.5	4.9	960	2 S72824	DNA-directed RNA p
C:Accession: A37768	35	122.5	4.9	1146	2 A89922	conserved hypothet
R:Hauser, A.R.; Schlievert, P.M.	36	120.1	4.8	1892	2 H95076	zinc metalloprote
C:Accession: A37768	37	120.1	4.8	1892	2 H95076	hypothetical prote
R:Hauser, A.R.; Schlievert, P.M.	38	120.5	4.8	2401	2 T28676	hypothetical prote
C:Accession: A37768	39	119	4.8	351	2 D89991	hypothetical prote
R:Hauser, A.R.; Schlievert, P.M.	40	118	4.7	1306	2 T28133	OAE MSV152 probab
C:Accession: A37768	41	117	4.7	675	2 S16624	panc11lin-binding
R:Hauser, A.R.; Schlievert, P.M.	42	117	4.7	1186	2 C64588	ceag pathogenicity
C:Accession: A37768	43	116.5	4.7	770	2 B48910	desmocoilin 1a pre
R:Hauser, A.R.; Schlievert, P.M.	44	116.5	4.7	770	2 B48910	desmocoilin 1a pre
C:Accession: A37768	45	116.5	4.7	840	2 I37281	ducta precursor -

Query Match 53.1%; Score 1327.5; DB 2; Length 398;  
Best Local Similarity 91.5%; Pred. No. 1.4e-79;  
Matches 258; Conservative 5; Mismatches 8; Indels 11; Gaps 5;

132 FPGSKATATYEDNEDLSNTQILEYTT--KQPVKSLDSNGIRHOGNPPKLLTPV 248	132 FPGSKATATYEDNEDLSNTQILEYTT--KQPVKSLDSNGIRHOGNPPKLLTPV 248
133 FPGSKATATYEDNEDLSNTQILEYTT--KQPVKSLDSNGIRHOGNPPKLLTPV 173	133 FPGSKATATYEDNEDLSNTQILEYTT--KQPVKSLDSNGIRHOGNPPKLLTPV 173
134 FPGSKATATYEDNEDLSNTQILEYTT--KQPVKSLDSNGIRHOGNPPKLLTPV 173	134 FPGSKATATYEDNEDLSNTQILEYTT--KQPVKSLDSNGIRHOGNPPKLLTPV 173
249 EYVKRSGRSPFGQHAAGVCATATQAIKHYHFNMGKLYTTLSSNPFPHKMKLPA 308	249 EYVKRSGRSPFGQHAAGVCATATQAIKHYHFNMGKLYTTLSSNPFPHKMKLPA 308
174 EYVKRSGRSPFGQHAAGVCATATQAIKHYHFNMGKLYTTLSSNPFPHKMKLPA 233	174 EYVKRSGRSPFGQHAAGVCATATQAIKHYHFNMGKLYTTLSSNPFPHKMKLPA 233
309 AISTROYNNNTTTPYSGRENNQVMAISLMAVGVISVMDYGRSGSSAGSSRQAK 368	309 AISTROYNNNTTTPYSGRENNQVMAISLMAVGVISVMDYGRSGSSAGSSRQAK 368
234 AISTROYNNNTTTPYSGRENNQVMAISLMAVGVISVMDYGRSGSSAGSSRQAK 293	234 AISTROYNNNTTTPYSGRENNQVMAISLMAVGVISVMDYGRSGSSAGSSRQAK 293
369 ENFGYNSVQIRNSDPS--QDMENQIDKELSONPPTYQG--GKVGGAIFVDAQGNNFY 426	369 ENFGYNSVQIRNSDPS--QDMENQIDKELSONPPTYQG--GKVGGAIFVDAQGNNFY 426
294 ENFGYNSVQIRNSDPS--QDMENQIDKELSONPPTYQG--GKVGGAIFVDAQGNNFY 353	294 ENFGYNSVQIRNSDPS--QDMENQIDKELSONPPTYQG--GKVGGAIFVDAQGNNFY 353
427 FVNNKGNGVSKDFPDLAINTSLALGTGGAGGFGTOSAVNG 468	427 FVNNKGNGVSKDFPDLAINTSLALGTGGAGGFGTOSAVNG 468
354 FVNNKGNGVSKDFPDLAINTSLALGTGGAGGFGTOSAVNG 395	354 FVNNKGNGVSKDFPDLAINTSLALGTGGAGGFGTOSAVNG 395

## RESULT 2

streptococcal pyrogenic exotoxin B precursor - Streptococcus pyogenes  
N:Alternate names: streptococcal cysteine proteinase; streptococcal peptidase A  
C:Species: Streptococcus pyogenes  
C:Date: 24-Apr-1984 #sequence-revision 07-Oct-1994 #text-change 07-Oct-1994  
C:Accession: S07668; A00978; L0017  
C:Title: S.D.; Lau, T.Y.  
C:Journal: J. Biol. Chem., 1982  
C:Protein Chem., 1, 317-334, 1982

A:Molecule type: DNA  
A:Residues: 9-244 <MEM>  
A:Cross-references: EMBL:X61556; NID:g47291; PIDN:CAA3754.1; PTD:g47292  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1998

A:Accession: S18785  
A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 9-244 <MEM>  
A:Cross-references: EMBL:X61559; NID:g47293; PIDN:CAA3757.1; PTD:g47294  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1998

A:Accession: S18791  
A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 9-244 <MEM>  
A:Cross-references: EMBL:X61555; NID:g47309; PIDN:CAA3753.1; PTD:g47310  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1998

A:Accession: S18795  
A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 9-244 <MEM>  
A:Cross-references: EMBL:X61557; NID:g47319; PIDN:CAA3755.1; PTD:g47320  
A:Experimental source: Streptococcus pyogenes strain M6A5493 isolate France unassigned

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1998

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 9-244 <MEM>  
A:Cross-references: EMBL:X61558; NID:g47321; PIDN:CAA3756.1; PTD:g47322  
A:Experimental source: Streptococcus pyogenes strain M6A5494 isolate France unassigned

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1998

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 9-228 <MEM>  
A:Cross-references: EMBL:X61554; NID:g47327; PIDN:CAA3752.1; PTD:g47328  
A:Experimental source: Streptococcus pyogenes strain M6A5500 isolate New Zealand unassigned

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1998

C:Gene(s): speA  
C:Cistron(s)  
C:Superfamily: enterotoxin B  
C:Keywords: exotoxin  
F:1-251/Product: exotoxin type A status predicted <MAY>

Query Match      45.2%    Score 1129    DB:1    Length 251:  
Best Local Similarity    97.7%    Seq-ID %    67.2  
Matches    216;    Conservative    1;    Mismatches    2;    Indels    2;    Gaps    2;

Oy                 2 OODPDSQHSRLSKVKNLONTFLYFGSPPTHEHNVKSVDOALSHSLLYNVSPPVDTOKT 61  
Db                 31 OODPDSQHSRLSKVKNLONTFLYFGSPPTHEHNVKSVDOALSHSLLYNVSPPVDTOKT 90

Oy                 6 ELKNDQMAETLKQNKMDITIGVEYHYHCLEDAENERSACTGCTYREGSNHLETFPKTYIK 120  
Db                 91 ELKNDQMAETLKQNKMDITIGVEYHYHCLEDAENERSACTGCTYREGSNHLETFPKTYIK 150

Oy                 121 VSIIOGIOSLPEDLETNNKKWVRNOADLYVKRYILDNNOLYNPSCKEKGVIKRFPRKKE 180  
Db                 131 VSIIOGIOSLPEDLETNNKKWVRNOADLYVKRYILDNNOLYNPSCKEKGVIKRFPRKKE 210

Oy                 181 SFMEDFPPEPTQSXTLYATNDETLDNST-QIEVYLTRYK 220  
Db                 211 SFMEDFPPEPTQSXTLYATNDETLDNSTQIEVYLTRYK 251

RESULT 4  
S18783  
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain M6A516  
N:Alternate names: scarlet fever toxin  
N:Species: Streptococcus pyogenes phage



62 ELKNDMAATLFKNDKNDVIGVEYHYHLCYCENMERSACI-GGVTNRSGNHLIEPRKIYVK 120  
 Db 83 ELKNDMAATLFKNDKNDVIGVEYHYHLCYCENMERSACI-GGVTNRSGNHLIEPRKIYVK 142  
 Oy 121 VSIDIGLSFDIEFNKKNVTAQAEIDYKRRKNTLNKQLTNPGSKYETGYIIFPNKESFV 180  
 Db 143 VSIDIGLSFDIEFNKKNVTAQAEIDYKRRKNTLNKQLTNPGSKYETGYIIFPNKESFV 202  
 Oy 181 SFMFDFPEPFETOSKLYMTIKNDLTDSNT 211  
 Db 203 SFMFDFPEPFETOSKLYMTIKNDLTDSNT 233  
 RESULT 6  
 518789  
 exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGA5262 isolate Calliope)  
 M.ALternate names: scarlet fever toxin  
 C.Species: Streptococcus pyogenes  
 A.Variant: Strain MGA5262 isolate Calliope  
 C.Date: 10-Sep-1999 #sequence\_revision 29-Jan-1993 #extl\_change 16-Jul-1999  
 R.Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.  
 J. Exp. Med. 174, 1271-1274, 1991  
 A.Title: Characterization and clonal distribution of four alleles of the speA gene encoded by the exotoxin A precursor of Streptococcus pyogenes  
 A.Reference number: 518782; MID:9204323; PMID:1940804  
 A.Cross-references: EMBL:X61573; MID:947303; PID:CA43771.1; PID:947304  
 A.Residues: 1-236 <NLS>  
 A.Molecule type: DNA  
 A.Note: The nucleotide sequence was submitted to the EMBL Data Library, September 1991  
 C.Genetics:  
 A.Gene: speA  
 A.Locus: 1.1; enterotoxin B  
 C.Reports: exotoxin  
 F.1-2/Domain: signal sequence (fragment) #status predicted <SIG>  
 F.23-236/Product: exotoxin A (fragment) #status predicted <NLS>  
 Query Match 39.5%; Score 986.5; DB 2; Length 236;  
 Best Local Similarity 88.2%; Pred. No. 1.3e-57;  
 Matches 186; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
 Oy 2 GOOPDPSLRSLVYNKQNTFYFLBEDPVHNKMSQDLNSHDITVNSGPNWDKLT 61  
 Db 23 GOOPDPSLRSLVYNKQNTFYFLBEDPVHNKMSQDLNSHDITVNSGPNWDKLT 82  
 Oy 62 ELKNDMAATLFKNDKNDVIGVEYHYHLCYCENMERSACI-GGVTNRSGNHLIEPRKIYVK 120  
 Db 83 ELKNDMAATLFKNDKNDVIGVEYHYHLCYCENMERSACI-GGVTNRSGNHLIEPRKIYVK 142  
 Oy 121 VSIDIGLSFDIEFNKKNVTAQAEIDYKRRKNTLNKQLTNPGSKYETGYIIFPNKESFV 180  
 Db 143 VSIDIGLSFDIEFNKKNVTAQAEIDYKRRKNTLNKQLTNPGSKYETGYIIFPNKESFV 202  
 Oy 181 SFMFDFPEPFETOSKLYMTIKNDLTDSNT 211  
 Db 203 SFMFDFPEPFETOSKLYMTIKNDLTDSNT 233  
 RESULT 7  
 A26152  
 streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.  
 M.ALternate names: scarlet fever toxin; SPE type A (speA)  
 C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #extl\_change 10-Sep-1999  
 C.Accession: A26152  
 R.Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.  
 Mol. Gen. Genet. 203, 334-356, 1986  
 A.Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus exotoxin A  
 A.Reference number: A26152; MID:86284313; PMID:3526093  
 A.Molecule type: DNA

A.Residues: 1-250 <JOB>  
 C.Superfamily: enterotoxin B  
 C.Keywords: exotoxin  
 Query Match 37.5%; Score 938.5; DB 1; Length 250;  
 Best Local Similarity 84.5%; Pred. No. 2.3e-54;  
 Matches 185; Conservative 5; Mismatches 25; Indels 3; Gaps 3;  
 Oy 5 PDPSLRSLVYNKQNTFYFLBEDPVHNKMSQDLNSHDITVNSGPNWDKLT 64  
 Db 34 PKPSDLSFDIEFNKKNVTAQAEIDYKRRKNTLNKQLTNPGSKYETGYIIFPNKESFV 93  
 Oy 65 NQMAATLFKNDKNDVIGVEYHYHLCYCENMERSACI-GGVTNRSGNHLIEPRKIYVK 123  
 Db 94 NQMAATLFKNDKNDVIGVEYHYHLCYCENMERSACI-GGVTNRSGNHLIEPRKIYVK 153  
 Oy 124 DGISGLSFDIEFNKKNVTAQAEIDYKRRKNTLNKQLTNPGSKYETGYIIFPNKESFV 183  
 Db 154 DGISGLSFDIEFNKKNVTAQAEIDYKRRKNTLNKQLTNPGSKYETGYIIFPNKESFV 212  
 Oy 184 PDPEPFETOSKLYMTIKNDLTDSNT-GIEVYITTK 220  
 Db 213 PDPEPFETOSKLYMTIKNDLTDSNTGIEVYITTK 250  
 RESULT 8  
 518786  
 enterotoxin B precursor - Staphylococcus aureus  
 C.Species: Staphylococcus aureus  
 C.Date: 24-Apr-1984 #sequence\_revision 15-Oct-1996 #extl\_change 18-Jun-1999  
 C.Accession: S27260; A92065; S27240; M01815  
 R.Jones, C.L.; Khan, S.A.  
 J. Bacteriol. 166, 29-33, 1986  
 A.Title: Molecular cloning and characterization of the enterotoxin B gene from Staphylococcus aureus.  
 A.Reference number: S27260; MID:86168029; PMID:357869  
 A.Cross-references: EMBL:M1118; MID:g152999; PID:MAA8850.1; PID:g153000  
 A.Residues: 1-266 <JOB>  
 A.Molecule type: DNA  
 A.Note: The nucleotide sequence was submitted to the EMBL Data Library, September 1984  
 C.Genetics:  
 A.Gene: enterotoxin B  
 A.Locus: 1.1; enterotoxin B  
 C.Reports: enterotoxin B  
 F.1-2/Domain: signal sequence (fragment) #status predicted <SIG>  
 F.23-236/Product: enterotoxin B (fragment) #status predicted <NLS>  
 Query Match 39.5%; Score 986.5; DB 2; Length 236;  
 Best Local Similarity 88.2%; Pred. No. 1.3e-57;  
 Matches 186; Conservative 13; Mismatches 11; Indels 1; Gaps 1;  
 Oy 2 GOOPDPSLRSLVYNKQNTFYFLBEDPVHNKMSQDLNSHDITVNSGPNWDKLT 61  
 Db 23 GOOPDPSLRSLVYNKQNTFYFLBEDPVHNKMSQDLNSHDITVNSGPNWDKLT 82  
 Oy 62 ELKNDMAATLFKNDKNDVIGVEYHYHLCYCENMERSACI-GGVTNRSGNHLIEPRKIYVK 120  
 Db 83 ELKNDMAATLFKNDKNDVIGVEYHYHLCYCENMERSACI-GGVTNRSGNHLIEPRKIYVK 142  
 Oy 121 VSIDIGLSFDIEFNKKNVTAQAEIDYKRRKNTLNKQLTNPGSKYETGYIIFPNKESFV 180  
 Db 143 VSIDIGLSFDIEFNKKNVTAQAEIDYKRRKNTLNKQLTNPGSKYETGYIIFPNKESFV 202  
 Oy 181 SFMFDFPEPFETOSKLYMTIKNDLTDSNT 211  
 Db 203 SFMFDFPEPFETOSKLYMTIKNDLTDSNT 233  
 RESULT 9  
 A26152  
 streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.  
 M.ALternate names: scarlet fever toxin; SPE type A (speA)  
 C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #extl\_change 10-Sep-1999  
 C.Accession: A26152  
 R.Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.  
 Mol. Gen. Genet. 203, 334-356, 1986  
 A.Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus exotoxin A  
 A.Reference number: A26152; MID:86284313; PMID:3526093  
 A.Molecule type: DNA









**THIS PAGE BLANK (USPTO)**